

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 09:57:42 : Search time 4967 seconds

(without alignments)

13384.835 Million cell updates/sec

Title: US-09-931-157-1

Perfect score: 4105

Sequence: 1 gaattcggcgccgtcttg.....taaaagttacagaacatt 4105

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

sarched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_mam:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	797.8	19.4	865	9	AU118882	AU118882 AU118882
2	792.2	19.3	863	9	AU119546	AU119546 AU119546
3	789	19.2	869	9	AU120519	AU120519 AU120519
c 4	725.6	17.7	781	9	A1936539	A1936539 wd29b09.x
5	710.4	17.3	733	14	BM719244	BM719244 UI-E-E01-
c 6	704.2	17.2	777	14	BQ018994	BQ018994 UI-H-DH1-

7	695.8	17.0	764	9	AU139639	AU139639 AU139639
8	694.4	16.9	739	9	AI694278	AI694278 wd45a01.x
c 9	692.2	16.9	732	14	BQ575745	BQ575745 UI-H-E21-
c 10	687.8	16.8	747	9	AI809396	AI809396 wf70b01.x
c 11	685	16.7	705	14	BQ006584	BQ006584 UI-H-E11-
c 12	683	16.6	742	12	BG116534	BG116534 602317635
c 13	683	16.6	771	12	BG695989	BG695989 602679314
c 14	673	16.4	677	9	AI130721	AI130721 qcl6el2.x
c 15	653.4	15.9	724	9	AI953824	AI953824 wx69h09.x
c 16	650.6	15.8	1072	13	BM548868	BM548868 AGENCOURT
c 17	649.8	15.8	708	9	AU117099	AU117099 AU117099
c 18	640.8	15.6	1627	11	AK017486	AK017486 Mus muscu
c 19	627	15.3	700	9	AI913052	AI913052 tz75f01.x
c 20	621.6	15.1	678	9	AI804414	AI804414 tc71a03.x
c 21	611	14.9	652	12	BF984079	BF984079 602307535
c 22	610	14.9	637	14	BM998050	BM998050 UI-H-DT1-
c 23	603.2	14.7	1043	12	BG114663	BG114663 602315469
c 24	603	14.7	621	14	BM683196	BM683196 UI-E-E01-
c 25	596.8	14.5	918	12	BF980903	BF980903 602304437
c 26	595.4	14.5	674	9	AI417092	AI417092 tg78905.x
c 27	595	14.5	595	13	BM512298	BM512298 ij70c02.x
c 28	582.2	14.2	645	12	BE813325	BE813325 RC3-BN003
c 29	569	13.9	609	10	BE328379	BE328379 hs93q06.x
c 30	563.2	13.7	676	12	BG548379	BG548379 602575155
c 31	561.8	13.7	582	9	AI144480	AI144480 qb72e08.x
c 32	552.6	13.5	572	9	AI240165	AI240165 qb39f10.x
c 33	534.8	13.0	595	9	AA234178	AA234178 zr49f02.r
c 34	534.4	13.0	560	9	AU145859	AU145859 AU145859
c 35	525.8	12.8	553	9	AL692187	AL692187 DKF7p313C
c 36	524.8	12.8	597	9	AU145342	AU145342 AU145342
c 37	521	12.7	580	9	AA452627	AA452627 zx33f03.r
c 38	520.4	12.7	554	9	AI252673	AI252673 qh86c11.x
c 39	519.6	12.7	660	9	AA910453	AA910453 oj89h09.s
c 40	516.4	12.6	524	9	AI332625	AI332625 qg28b02.x
c 41	514.4	12.5	552	9	AU158110	AU158110 AU158110
c 42	513.8	12.5	599	9	AA058926	AA058926 z196f11.r
c 43	513.2	12.5	563	9	AA406195	AA406195 zv24d09.s
c 44	512.4	12.5	664	9	AU116816	AU116816 AU116816
c 45	512.2	12.5	549	9	AI475501	AI475501 tj92h05.x

ALIGNMENTS

RESULT 1	AU118882	865 bp	linear	EST 01-AUG-2002
LOCUS	AU118882	HEMBAL Homo sapiens	cdna clone HEMBAL004569 5', mRNA	
DEFINITION	AU118882	sequence.		
ACCESSION	AU118882			
VERSION	AU118882.1	GI:10934117		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 865)			
AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isozaki, T.			
TITLE	HRI human cdna project			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cdna project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cdna library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.			

FEATURES	source	Location/Qualifiers
Db	841	CNCNTAGTTTGAAAAAAGGAC 864
RESULT 2		
LOCUS	AU119546	
DEFINITION	AU119546 HEMBA1 Homo sapiens cdna clone HEMBA1006071 5', mRNA	EST 01-AUG-2002
ACCESSION	AU119546	
VERSION	AU119546	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
TITLE		HRI human cdna project
JOURNAL		Unpublished (2000)
COMMENT		Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cdna project: 5'- & 3'-end one pass sequencing: Helix Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES		Location/Qualifiers
		1. 863
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="HEMBA1006071"
		/clone_lib="HEMBA1"
		/tissue_type="whole embryo, mainly head"
		/dev_stage="embryo, 10 weeks"
		/note="vector: pME18SFL3"
BASE COUNT	285 a	130 c 130 g 316 t 2 others
ORIGIN		
Query Match	19.3%	Score 792.2; DB 9; Length 863;
Best Local Similarity	97.8%	Pred. No. 8.5e-168;
Matches	845;	Conservative 0; Mismatches 14; Indels 5; Gaps 4;
Qy	2045	GAACACCAAGGATTTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGGCTAG 2104
Db	1	GAACACCAAGGATTTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGGCTAG 60
Qy	2105	CTTTTATGGCAGTTCTGCTGAATGTTCAATGGAACTGGTCAACATGAACCTTTAGAGAT 2164
Db	61	CTTTTATGGCAGTTCTGCTGAATGTTCAATGGAACTGGTCAACATGAACCTTTAGAGAT 120
Qy	2165	TAACGACAAAGATTTTCTACTTTTAAAGTGA--TTTGTGCTTCAGCCCAACACCAAT 2222
Db	121	TAACGACAAAGATTTTCTACTTTTAAAGTGA--TTTGTGCTTCAGCCCAACACCAAT 180
Qy	2223	ATGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGGCCAGTATTTTAACTGCATA 2282
Db	181	ATGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGGCCAGTATTTTAACTGCATA 240
Qy	2283	ATAGCTAACATGATTTATTTGAACCTTTTACACATAGTTTGAACCAAGGACCAAAA 2342
Db	241	ATAGCTAACATGATTTATTTGAACCTTTTACACATAGTTTGAACCAAGGACCAAAA 299
Qy	2343	TAGTATTCAGGTGAGCAATAGATTAGTTTCCACCTCACTATTTATTTTAAAC 2402
Db	300	TAGTATTCAGGTGAGCAATAGATTAGTTTCCACCTCACTATTTATTTTAAAC 359


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DEFINITION wd29b09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2329529 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI936539
VERSION AI936539.1 GI:5675409
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 781)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 1132 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
FEATURES
     1..781
         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="IMAGE:2329529"
         /clone_lib="Soares_NFL_T_GBC_S1"
         /lab_host="DH10B"
         /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
         a modified polylinker; Site_1: Not I; Site_2: Eco RI;
         Equal amounts of plasmid DNA from three normalized
         libraries (fetal lung NBHL19W, testis NHT, and B-cell
         NCI CGAP GCBI) were mixed, and ss circles were made in
         vitro. Following HAP purification, this DNA was used as
         tracer in a subtractive hybridization reaction. The driver
         was PCR-amplified cDNAs from pools of 5,000 clones made
         from the same 3 libraries. The pools consisted of
         I.M.A.G.E. clones 297480-302087, 682632-687239,
         726408-728711, and 729096-731399. Subtraction by Bento
         Soares and M. Fatima Bonaldo.
         264 a 154 c 129 g 232 t 2 others
BASE COUNT 264 a 154 c 129 g 232 t
ORIGIN
Query Match 17.7%; Score 725.6; DB 9; Length 781;
Best Local Similarity 97.1%; Pred. No. 8.8e-153;
Matches 748; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 3336 CAACCTGCCCTCAGTCCATTTTAACTCTGTAGCAACCTTTCTGCATTTCATTAATCTGTAAATC 3395
|||||
773 CAAACAGCTTCAGTCCATTTT-ACCTGTAGCAACCGTCTGCATTTCATTAATCTGTAGTGC 715

QY 3396 ATGTTACCATCAAAATGGGATATAAGCAGCGCGTGAACGAGATGAGCTGTGGACTAG 3455
|||||
714 ATGTACCATTCACNAATGGGATATAAGCAGCGCGTGAACGAGATGAGCTGTGGACTAG 655

QY 3456 CAATATAGGGTTTGTGTTGGTGTGCTGTGATTAAGCAGCTATTGGGGTCATATGTT 3515
|||||
654 CAATATAGGGTTTGTGTTGGTGTGCTGTGATTAAGCAGCTATTGGGGTCATATGTT 595

QY 3516 TCCTGTCTGGAGCAAAAGTCATTACACTTTGAAGTATTATATGTTCTTATCTCAATT 3575
|||||
594 TCCTGTCTGGAGCAAAAGTCATTACACTTTGGAGTATTATATGTTCTTATCTCAATT 535

QY 3576 CAATGTGGTGATGAAATGGCAGGTGCTGTGATATTTCTTTCAGACTTCGCCAGACAGAT 3635
|||||
534 CAATGTGGTGATGAAATGGCAGGTGCTGTGATATTTCTTTCAGACTTCGCCAGACAGAT 475

QY 3636 TCGTGATAAATAATAGTAGTAAGATAATTTGTTGGGCCATATTTTAGACAGCGTAAATAA 3695
|||||
474 TCGTGATAAATAATAGTAGTAAGATAATTTGTTGGGCCATATTTTAGACAGCGTAAATAA 415

QY 3696 CATCAGGTTCCAGTTGCTTGAATTCGAAGCTAGAGAGTACTGCCCTTTTGTGTGTTAGC 3755

```

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Db 414 CATCAGGTTCCAGTTGCTTGAATTCGAAGCTAGAGTACTGCCCTTTTGTGTGTTAGC 355
|||||
QY 3756 AGTCAAAATCTATTATTCCTACTGGCGCATCATATGCGAGTGATATATGCTATATATAGC 3815
|||||
Db 354 AGTCAAAATCTATTATTCCTACTGGCGCATCATATGCGAGTGATATATGCTATATATAGC 295
|||||
QY 3816 CATAGGTTCCACACCAATTTGTTTAGACAATGTCCTTTTTCAGATGCTTTGTTCTTTT 3875
|||||
Db 294 CATAGGTTCCACACCAATTTGTTTAGACAATGTCCTTTTTCAGATGCTTTGTTCTTTT 235
|||||
QY 3876 CATATGAAAAAATGCAATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGCGCTCAACG 3935
|||||
Db 234 CATATGAAAAAATGCAATTTTATAAATTCAGAAAGTCATAGATTTCTGAAGCGCTCAACG 175
|||||
QY 3936 TGCATTTTATTATGACGACGTTAACTGTTGTTTACTAGCAGGAATATTTCCCAATTT 3995
|||||
Db 174 TGCATTTTATTATGACGACGTTAACTGTTGTTTACTAGCAGGAATATTTCCCAATTT 115
|||||
QY 3996 CTACCTTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCAGAGCCAGGCC 4055
|||||
Db 114 CTACCTTTTACTACATCTTTTCAACAAGTAACTTTGTAGAAATGAGCAGAGCCAGGCC 55
|||||
QY 4056 CTGAGTTGGCAGTGGCCCATAGTGTAAATAAAGTTTACAGAAACCTT 4105
|||||
Db 54 CTGAGTTGGCAGTGGCCCATAGTGTAAATAAAGTTTACAGAAACCTT 5
|||||

RESULT 5
BM719244
LOCUS BM719244 733 bp mRNA linear EST 01-MAR-2002
DEFINITION UI-E-E01-ajd-b-04-0-UI.r1 UI-E-E01 Homo sapiens cDNA clone
UI-E-E01-ajd-b-04-0-UI 5', mRNA sequence.
ACCESSION BM719244
VERSION BM719244.1 GI:19037818
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 733)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
     1..733
         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="UI-E-E01-ajd-b-04-0-UI"
         /clone_lib="UI-E-E01"
         /tissue_type="fetal eye"
         /dev_stage="fetal"
         /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
         /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
         modified polylinker; Site_1: EcoR I; Site_2: Not I;
         UI-E-E01 is a normalized cDNA library containing the
         following tissue(s): fetal eye. The library was

```


Constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is CGCTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NET).

BASE COUNT	199 a	115 c	150 g	267 t	2 others
ORIGIN					
Query Match	17.3%; Score 710.4; DB 14; Length 733;				
Best Local Similarity	99.4%; Pred. No. 2.3e-149;				
Matches	722;	Conservative	0;	Mismatches	3; Indels 1; Gaps 1;
3162	TGTAAATTTCTTTAGCCATTTTCTAGACTGTCTCTGTGGAATATATTTGTGTGTG 3221				
Db	TT 60				
3222	ATATATGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3281				
Db	TT 61				
3282	AGTTGTGCAAGTGCATGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 3341				
Db	TT 121				
3342	GCCTCAGTCCATTTTAACTGTAGCACTCTCTGATTCATTAATCTTGTATCATGTGA 3401				
Db	TT 180				
3402	CCATTCAAAATGGATATAGAGCGAGCGTGAAGAGAGATGAGTGTGGACTAGCAATAT 3461				
Db	TT 240				
3462	AGGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3521				
Db	TT 300				
3522	GCTGGAGCAAAAGTCATTACACTTTGAAGTATTATTTGTTCTTATCTCTCAATCAATGT 3581				
Db	TT 360				
3582	GGTGATGAAATGCGAGGTTGCTGATATTTCTTTTCAGACTTCGCCAGACAGATTGCTGA 3641				
Db	TT 420				
3642	TAATAAATAGGTAAGATAATTTCTGGGCCATATTTTAGACAGGTAATAATACATCAG 3701				
Db	TT 480				
3702	GTTCAGTGTGCTGAAATGCAAGCTAAGAAGTACTGCCCTTTTGTGTTAGCAGTCAA 3761				
Db	TT 540				
3762	ATCTATATTTCCACTGGCGCATCATATGCGATGATATATGCTATATATAAGCCATAGG 3821				
Db	TT 600				
3822	TTACACCAATTTTGTAGCAATGCTTTTTTTTCAAGATGCTTTTCTTTTCATATG 3881				
Db	TT 660				
3882	AAAAAA 3887				
Db	TT 720				

RESULT 6

BQ018994/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BQ018994 777 bp mRNA linear EST 27-MAR-2002
 UI-H-DH1-awv-o-07-0-UI-s1 NCI-CGAP_DHI Homo sapiens cDNA clone
 IMAGE:5824350 3', mRNA sequence.
 BQ018994
 BQ018994.1 GI:19754271
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 777)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Seq primer: M13 FORWARD
 POLYA-Yes

Location/Qualifiers
 1. 777
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5824350"
 /clone_lib="NCI-CGAP_DHI"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DHI0B (Life Technologies)"
 /note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site:1; EcoR I; Site:2; Not I; NCI-CGAP_DHI is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTCG.
 TAG_LIB=UI-H-DHI
 TAG_TISSUE=Lung
 TAG_SEQ=AGATCATTCG"

BASE COUNT 219 a 138 c 166 g 253 t 1 others
 ORIGIN

Query Match 17.2%; Score 704.2; DB 14; Length 777;
 Best Local Similarity 97.9%; Pred. No. 5.9e-148;
 Matches 734; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY	1595	TTTGTGAGCAAGAAATTTAAATAATTTTCCAGTCATCCCTCTGCTGCTGTGTACACG 1654
Db	750	TATWTGTGAGCAAGAAATTTAAATAATTTTCCAGTCATCCCTCTGCTGCTGTGTACACG 691
QY	1655	TCCAAAAGTCTGATGACCTCGGTCGCCATGAACGCAACAGCATCCAGTGGGAAGAACAC 1714
Db	690	TCCAAAAGTCTGATGACCTCGGTCGCCATGAACGCAACAGCATCCAGTGGGAAGAACAC 631
QY	1715	GATCAAAACCAACCAACACAGACCGGAGCGCATAGGACAGCATGAATGACATGACACCC 1774
Db	630	GATCAAAACCAACCAACACAGACCGGAGCGCATAGGACAGCATGAATGACATGACACCC 571
QY	1775	TTAGAACCATCTCTCGGTACTCCCATTAATCTCTCGGAGAAAAAATCAACAGCAACTG 1834

Db 570 TTAGAAGCACTCTCGGTACTCCCATATCTCTCGGAGAAAAAATACAAAGCAACTG 511
 QY 1835 TGACTCCGGGAATCTCTCTGATCCCTTCTCTTAAATCACTCCACACCAAGAAGA 1894
 Db 510 TGAGTCCGGGAATCTCTCTGATCCCTTCTCTTAAATCACTCCACACCAAGAAGA 451
 QY 1895 AATGCTTTCCAAAACCGCAA-GGTAGACTGGTTTATCCACCCACAACATCTAGCAATCGT 1953
 Db 450 AATGCTTTCCAAAACCGGAAGGTAGACTGGTTTATCCACCCACAACATCTAGCAATCGT 391
 QY 1954 ACTTCTTTAATGATCAATTTACATATTCTGGTGTGTGTTATTCAGCACTAAAAAATGGT 2013
 Db 390 ACTTCTTTAATGATCAATTTACATATTCTGGTGTGTGTTATTCAGCACTAAAAAATGGT 331
 QY 2014 GGGAGCTGGGGAGATGAAGACTGTTAAATGAACACAGAAGATATTACTACTTTTGC 2073
 Db 330 GGGAGCTGGGGAGATGAAGACTGTTAAATGAACACAGAAGATATTACTACTTTTGC 271
 QY 2074 ATGAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGCGAGTTCTGGTGAATGTTCAA 2133
 Db 270 ATGAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGCGAGTTCTGGTGAATGTTCAA 211
 Db 2134 TGGGAACCTGGTCACCATGAACCTTTAGAGATTAAACGACAAGATTTTCTACTTTTTTAAG 2193
 Db 210 TGGGAACCTGGTCACCATGAACCTTTAGAGATTAAACGACAAGATTTTCTACTTTTTTAAG 151
 QY 2194 TGA-TTTTGTGCTTCAGCCAAACAATATGGGTCAGGTCACATTTTATTTGAAATGT 2252
 Db 150 TGATTTTTTTGTGCTTCAGCCAAACAATATGGGTCAGGTCACATTTTATTTGAAATGT 91
 QY 2253 CATTTGGTGCCAGTATTTTAACTGCATATAGCCCTAACATGATTTTGAACCTTATTT 2312
 Db 90 CATTTGGTGCCAGTATTTTAACTGCATATAGCCCTAACATGATTTTGAACCTTATTT 31
 QY 2313 ACACATAGTTTGAACCAAAAAAGACAAAAA 2342
 Db 30 ACACATAGTTTGAACCAAAAAAGACAAAAA 1

RESULT 7
 LOCUS AUI39639 764 bp mRNA linear EST 05-AUG-2002
 DEFINITION AUI39639 PLACE1 Homo sapiens cDNA clone PLACE1011029 5', mRNA
 sequence.

ACCESSION AUI39639
 VERSION AUI39639.1 GI:11001160
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 764)
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
 Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 Isogai,T.
 HRI human cDNA project
 Unpublished (2000)
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 Location/Qualifiers
 1. 764
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="PLACE1011029"

TITLE
 JOURNAL
 COMMENT

FEATURES
 source

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 /notes="Vector: pME18SFL3"
 BASE COUNT 252 a 134 c 111 g 263 t 4 others
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 Best Local Similarity 97.6%; Pred. No. 4.6e-146;
 Matches 726; Conservative 0; Mismatches 15; Indels 3; Gaps 2;
 QY 2322 TTCAAAAAAGACAAAAATAGTATTTCAGGTGAGCAATAGATTAGTATTTTCCACGT 2381
 Db 5 TTTGAAAAAAGACAAAAATAGTATTTCAGGTGAGCAATAGATTAGTATTTTCCACGT 64
 QY 2382 CACTATTATTATTTTAAAAACACAAATCTTAAAGCTACAACAATACTACAGGCCCTTAA 2441
 Db 65 CACTGTTTATTTTAAAAACACAAATCTTAAAGCTACAACAATACTACAGGCCCTTAA 124
 QY 2442 AGCACAGTCTGATGACACATTTGGCAGTTTAAATAGATGTTTACTCAAAAGATTTTAA 2501
 Db 125 AGCACAGTCTGATGACACATTTGGCAGTTTAAATAGATGTTTACTCAAAAGATTTTAA 184
 QY 2502 ACTGTATTTTATTTTAAATGCTTTTATTACAGGGGACCTTGAACATGTTTGTATG 2561
 Db 185 ACTGTATTTTATTTTAAATGCTTTTATTACAGGGGACCTTGAACATGTTTGTATG 244
 QY 2562 TTAATATCAAAAGCTAATGCTTCAATCAGATAGTTCCTTTTTCACAAAGTTCAATCTGTTT 2621
 Db 245 TTAATATCAAAAGCTAATGCTTCAATCAGATAGTTCCTTTTTCACAAAGTTCAAT-CTGTTT 303
 QY 2622 TCAATGTAATTTTGTATGAAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAT 2681
 Db 304 TCAATGTAATTTTGTATGAAAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGTCAT 363
 QY 2682 TTAACCTCGCTGAGACTTTTCAGTGCACCTGTATATAGAACTTAAACACACCTAAAGA 2741
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 Db 544 AGTAAGTCTTTTGTGATCATCTCCCTTTTCCATATAGGAAACATAATTTTGAAGTGGCCAG 603
 QY 2922 ATGAGTTTATCATGTGAGTGAATAAATTAATCCACAAATGCCACCAAGTAACCTTAACGAT 2981
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 DEFINITION IMAGE:231048 3' similar to gb:S57498 ENDOTHELIN-1 RECEPTOR
 PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION A1694278
 VERSION A1694278.1 GI:4971618
 KEYWORDS EST.
 SOURCE human.

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ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 739)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               This clone is available royalty-free through LNL; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Insert Length: 1706 Std Error: 0.00
               Seq primer: -400P from Gibco
               High quality sequence stop: 458.
               Location/Qualifiers
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               /lab_host="DH10B"
               /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
               a modified polylinker; Site_1: Not I; Site_2: Eco RI;
               Equal amounts of plasmid DNA from three normalized
               libraries (fetal lung NBHL19W, testis NHT, and B-cell
               NCI-CGAP_GCB1) were mixed, and ss circles were made in
               vitro. Following HAP purification, this DNA was used as
               tracer in a subtractive hybridization reaction. The driver
               was PCR-amplified cDNAs from pools of 5,000 clones made
               from the same 3 libraries. The pools consisted of
               I.M.A.G.E. clones 297480-302087, 682632-687239,
               726408-728711, and 729096-731399. Subtraction by Bento
               Soares and M. Fatima Bonaldo.
BASE COUNT     252 a 148 c 120 g 219 t
ORIGIN
Query Match    16.9%; Score 694.4; DB 9; Length 739;
Best Local Similarity 98.2%; Pred. No. 9.5e-146;
Matches 723; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 3370 CTTCTGCTCATTAATCTTGTATATGTTTACCATTACAAATGGGATATAGAGGCACG 3429
Db 739 CTTCCGCGATTCTAT-ATCTCTGTTATGTTT-CCTTCCAAATGGGATATAGAGGCACG 682
QY 3430 GTGAAGCAGATGACCTGTGACATAGCAATATAGGTTTGTGTTGGTGGTTGGAT 3489
b 681 GTGAAGCAGATGACCTGTGACATAGCAATATAGGTTTGTGTTGGTGGTTGGAT 622
QY 3490 AAAGCAGTATTGGGGTCATATTTCTCTGCTGGAGCAAAAGTCATTACACTTTTCAA 3549
Db 621 AAAGCAGTATTGGGGTCATATTTCTCTGCTGGAGCAAAAGTCATTACACTTTGAAA 562
QY 3550 GTATTATATGTTCTTATTCCTCAATCAATGTTGATGAATGCCAGGTTGTTGATGA 3609
Db 561 GTATTATATGTTCTTATTCCTCAATCAATGTTGATGAATGCCAGGTTGTTGATGA 502
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Db 501 TTCTTTTTCAGCTTCGCCACAGACATTCCTGATATATTAATAGGTAGATTAATTTGTTGG 442
QY 3670 GCCATATTTTAGGACAGTAAATTAACATCAGGTTCCAGTTGCTTGAATTCAGGCTAA 3729
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QY 3730 GAAGTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACATGGCCCATCATATG 3789
Db 381 GAAGTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACATGGCCCATCATATG 322
QY 3790 CAGTGATATATGCTTATATATATAGCCATAGGTTTCACACCATTTTGTGTTAGACAATGTC 3849
Db 321 CAGTGATATATGCTTATATATATAGCCATAGGTTTCACACCATTTTGTGTTAGACAATGTC 262

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QY 3850 TTTTTCACAGATGCTTTGCTTTCTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 3909
Db 261 TTTTTCACAGATGCTTTGCTTTCTTCATATGAAAAAATGCATTTTATAAATTCAGAAA 202
QY 3910 GTCATAGATTTCTGAAGCGTCACAGTCATTTTATTATGGAAGTGGTGAAGTAACTGTGG 3969
Db 201 GTCATAGATTTCTGAAGCGTCACAGTCATTTTATTATGGAAGTGGTGAAGTAACTGTGG 142
QY 3970 TTTTACTAGCAGCAATATTTTCCCAATTTCTACCTTTTACTACATCTTTTCAACAAGTAACTTT 4029
Db 141 TTTTACTAGCAGCAATATTTTCCCAATTTCTACCTTTTACTACATCTTTTCAACAAGTAACTTT 82
QY 4030 GTAGAAATGAGCCAGCAAGCCCTGAGTTGGCAGTGGCCCATAGTGTAAATAATAA 4089
Db 81 GTAGAAATGAGCCAGCAAGCCCTGAGTTGGCAGTGGCCCATAGTGTAAATAATAA 22
QY 4090 AGTTTACAGAAACCTT 4105
Db 21 AGTTTACAGAAACCTT 6

RESULT 9
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LOCUS      BQ575745              732 bp      mRNA      linear      EST 19-JUN-2002
DEFINITION      UI-H-E21-bbg-h-22-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA clone
                UI-H-E21-bbg-h-22-0-UI 3', mRNA sequence.
ACCESSION      BQ575745
VERSION        BQ575745.1 GI:21479062
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 732)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Dr. Steven Gitellis/ Rush Presbiterian, Dept. of
               Orthopaedics
               cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
               cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
               DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
               Clone Distribution: Clone distribution information can be obtained
               from Dr. M. Bento Soares, bento-soares@uiowa.edu
               Seq primer: M13 FORWARD
               POLYA=Yes.
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               /db_xref="taxon:9606"
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               /lab_host="DH10B (Life Technologies)"
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               NCI_CGAP_Ch2 is a normalized cDNA library containing the
               following tissue(s): Chondrosarcoma Grade II. The library
               was constructed according to Bonaldo, Lennon and Soares,
               Genome Research, 6:791-806, 1996. First strand cDNA
               synthesis was primed with an oligo-dT primer containing a
               Not I site. Double stranded cDNA was ligated to an EcoR I
               adaptor, digested with Not I, and cloned directionally
               into pT73-pac vector. The oligonucleotide used to prime
               the synthesis of first-strand cDNA contains a library tag
               sequence that is located between the Not I site and the
               (dT)18 tail. The sequence tag for this library is
               TGATCAGCT.
               TAG_LIB=UI-H-E21

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[illegible]

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Db 204 AAAGTCATAGATTTCTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAGTAACTG 145
Qy 3967 TGGTTTACTAGCAGGAATATTTCCAAATTTCTACCTTTTACTACATCTTTTCAACAAGTAAC 4026
Db 144 TGGTTTACTAGCAGGACTATTTCCAAATTTCTACCTTTTACTACATCTTTTCAACAAGTAAC 85
Qy 4027 TTTGTAGAAATGAGCCAGCAAGCCAAAGGCCCTGAGTTGGCAGTGGCCCATTAAGTGTAAAT 4086
Db 84 TTTGTAGAAATGAGCCAGCAAGCCAAAGGCCCTGAGTTGGCAGTGGCCCATTAAGTGTAAAT 25
Qy 4087 AAAAGTTTACAGAAACCTT 4105
Db 24 AAAAGTTTACAGAAACCTT 6

RESULT 11
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LOCUS
DEFINITION
ACCESSION
VERSION
BO006584
BO006584.1 GI:19731484
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 705)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap;
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
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Location/Qualifiers
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
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following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ACACTTGCAC.
TAG LIB=UT-H-E11
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC"
235 a 143 c 106 g 220 t 1 others
BASE COUNT
ORIGIN
Query Match
16.7%; Score 685; DB 14; Length 705;

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Best Local Similarity 99.9%; Pred. No. 1.2e-143;
Matches 685; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 705 AAGAGCGCGTCAAGCAGCATCAGCTGCGACTAGCAATATATAGGTTTGTGGTTGG 646
Qy 3480 TTGGTTTGATAAAGCAGTATTTGGGGTGCATATTTTCCCTGCTCGAGCAAAAGTCATT 3539
Db 645 TTGGTTTGATAAAGCAGTATTTGGGGTGCATATTTTCCCTGCTCGAGCAAAAGTCATT 586
Qy 3540 ACATTTTGAAGTATATATTTGTTCTTATCCTCAATTCATGCTGATGAATTTGCCAGG 3599
Db 585 ACATNTGAAGTATATATTTGTTCTTATCCTCAATTCATGCTGATGAATTTGCCAGG 526
Qy 3600 TTGCTCTGATATTTCTTCAGACTTCGCCAGACAGATGCTGATAATAAATAGTAAGAT 3659
Db 525 TTGCTCTGATATTTCTTCAGACTTCGCCAGACAGATGCTGATAATAAATAGTAAGAT 466
Qy 3660 AATTTGTTGGGCCATATTTTAGCAGAGTAAATAACATCAGGTTCCAGTTGCTTGAATT 3719
Db 465 AATTTGTTGGGCCATATTTTAGCAGAGTAAATAACATCAGGTTCCAGTTGCTTGAATT 406
Qy 3720 GCAAGGCTAAGAGTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACCTGGC 3779
Db 405 GCAAGGCTAAGAGTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACCTGGC 346
Qy 3780 GCATCATATGCAAGTATATGCTTATTAAGCAGTATGCTGATGATGATGATGATGATGAT 3839
Db 345 GCATCATATGCAAGTATATGCTTATTAAGCAGTATGCTGATGATGATGATGATGATGAT 286
Qy 3840 GACAATGCTCTTTTTCAGATGCTTTTCTTTTTCATATGATAAATAATGCAATTTTATA 3899
Db 285 GACAATGCTCTTTTTCAGATGCTTTTCTTTTTCATATGATAAATAATGCAATTTTATA 226
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Db 225 AATTCAGAAAGTCATAGATTTCTGAAGCGTCAACGTCATTTTATTTATGGACTGGTAA 166
Qy 3960 GTAACGTGGTTTACTAGCAGGAATATTTCCAAATTTTCTACCTTTACTACATCTTTCAAC 4019
Db 165 GTAACGTGGTTTACTAGCAGGAATATTTCCAAATTTTCTACCTTTACTACATCTTTCAAC 106
Qy 4020 AGTAACCTTTGAGAAATGAGCCAGCAAGCCAGGCGCTGAGTTGGCAGTGGCCCATAAAT 4079
Db 105 AGTAACCTTTGAGAAATGAGCCAGCAAGCCAGGCGCTGAGTTGGCAGTGGCCCATAAAT 46
Qy 4080 GTAAATATAAAGCTTTACAGAAACCTT 4105
Db 45 GTAAATATAAAGCTTTACAGAAACCTT 20

RESULT 12
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DEFINITION
602317635F1 NIH_MGC_88 Homo sapiens cDNA clone linear EST 30-JAN-2001
mRNA sequence.
ACCESSION
BG116534
VERSION
BG116534.1 GI:12610040
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/;
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10151 row: e column: 10
 High quality sequence stop: 697.

FEATURES

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 Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."
 BASE COUNT 166 a 211 c 208 g 157 t
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 Query Match 16.6%; Score 683; DB 12; Length 742;
 Best Local Similarity 97.1%; Pred. No. 3.5e-143;
 Matches 706; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
 QY 31 GTGGAGTGAAGGCTGGAGCTTTGGAGGAGACGGGAGGAGACTGGAGCGGTTC 90
 Db 1 GTGGAGTGAAGGCTGGAGCTTTGGAGGAGACGGGAGGAGACTGGAGCGGTTC 60
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 Db 181 TGGGTCCAGCGAGACCTCCCGGGAGAGAGAGTGCAGGAGTTTCTGAAGCGGG 240
 QY 271 GAAGTGTGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330
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 Db 301 CCACCCACCTCGCGCTTCTCTGCGCCAGCGCGCGCGCGCGCGCGCGCGCGCG 360
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RESULT 13

LOCUS BG699589 771 bp mRNA linear EST 07-MAY-2001
 DEFINITION 602679314F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4812050 5',
 mRNA sequence.
 ACCESSION BG699589
 VERSION BG699589.1 GI:13968056
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 771)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10703 row: 1 column: 03
 High quality sequence stop: 748.

FEATURES

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); Oligo-dT primed using primer 5'-ttttttttttttttt-3',
 size-selected for average insert size 2.5 kb and
 normalized to 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 182 a 224 c 198 g 167 t
 ORIGIN

Query Match 16.6%; Score 683; DB 12; Length 771;
 Best Local Similarity 97.4%; Pred. No. 3.5e-143;
 Matches 747; Conservative 0; Mismatches 15; Indels 5; Gaps 5;

QY 134 AGTCATCCCGCTGGTCTGACGATTGGAGAGCGGTGGAGAGCTTCATCCATCCACC 193
 Db 6 AGTCATCCCGCTGGTCTGACGATTGGAGAGCGGTGGAGAGCTTCATCCATCCACC 65
 QY 194 CGGTCTGCCCGGGATTGGGTCTCCAGCGACACCTCCCGGGAGAGAGAGTCCCGGAG 253
 Db 66 CGGTCTGCCCGGGACTGGGTCTCCAGCGACCTCCCGGGAGAGAGTCCCGGAGAG 125
 QY 254 AGTTTCTGAAGCGGGAGAGCTGTGCAGCGAAGCGCGCGCGCGCGCGCGCGGAC 313
 Db 126 AGTTTCTGAAGCGGGAGAGCTGTGCAGCGAAGCGCGCGCGCGCGCGCGGAC 185
 QY 314 ACCGCCACCTCCCGCGCCACCCACCTCGCTTCTTCTCGGCTTCTTCTGCGCCAGCGCC 373
 Db 186 ACCGCCACCTCCCGCGCCACCCACCTCGCGGCTCCGCGCTTCTTCTGCGCCAGCGCC 245

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 PRECURSOR (HUMAN); mRNA sequence.
 A1130721
 A1130721.1 GI:3600737
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 677)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapus-femail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by
 M. Fatima Bonaldo. This library was constructed from the
 same fetus as the fetal lung library, Soares fetal lung
 NBHH19W."

BASE COUNT 235 a 136 c 104 g 202 t
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 similar to gb:S57498 ENDOTHELIN-1 RECEPTOR PRECURSOR (HUMAN); mRNA
 sequence.
 724 bp mRNA linear EST 06-SEP-1999
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ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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					Contact: Robert Strausberg, Ph.D.				
					Email: cgapbs-r@mail.nih.gov				
					Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center				
					Cloned through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html				
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GenCore version 5.1.3
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Run on: December 12, 2002, 10:01:22 ; Search time 185 Seconds
(without alignments)
8774.959 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

searched: 355320 seqs, 197730502 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 1, Application US/09931157
; Patent No. US20020082414A1
; GENERAL INFORMATION:
; APPLICANT: Imura, Hiroo
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; NAME/KEY: sig_peptide
; LOCATION: (485)...(544)
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; LOCATION: (545)...(1768)
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 QY 1801 AATCTCTCGGAGAAAAAATCAAGGCAACTGTCACTCCGGGAATCTCTCTCTCATC 1860
 Db 1801 AATCTCTCGGAGAAAAAATCAAGGCAACTGTCACTCCGGGAATCTCTCTCTCATC 1860
 QY 1861 CTTCTTCTTAAATTCACCTCCACACCCCAAGAGAAATGCTTCCAAAACCGCAAGGTAGA 1920
 Db 1861 CTTCTTCTTAAATTCACCTCCACACCCCAAGAGAAATGCTTCCAAAACCGCAAGGTAGA 1920
 QY 1921 CTGGTTTATCCACCCACACATCTAGAAATGCTTCTTTAATTTGATCTAAATTTACATA 1980
 Db 1921 CTGGTTTATCCACCCACACATCTAGAAATGCTTCTTTAATTTGATCTAAATTTACATA 1980
 QY 1981 TTTCTGCTTGTGTATTCAGCACTTAAAAAATGGTGGAGCTGGGGGAGAAATGAAGACTGTT 2040
 Db 1981 TTTCTGCTTGTGTATTCAGCACTTAAAAAATGGTGGAGCTGGGGGAGAAATGAAGACTGTT 2040
 QY 2041 AAATGAACCCAGAGGATATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGG 2100
 Db 2041 AAATGAACCCAGAGGATATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGG 2100
 QY 2101 CTAGCTTTTATGGCAGTCTGTGTGAATGTTCAATGGGAATGCTGACCATGAACTTTAG 2160
 Db 2101 CTAGCTTTTATGGCAGTCTGTGTGAATGTTCAATGGGAATGCTGACCATGAACTTTAG 2160
 QY 2161 AGATTAAACGACAAGATTTCTACTTTTAAAGTGAATTTTGTCCCTCAGCCAAACACA 2220
 Db 2161 AGATTAAACGACAAGATTTCTACTTTTAAAGTGAATTTTGTCCCTCAGCCAAACACA 2220
 QY 2221 ATATGGCTCAGTCTACATTTTAAATTTGAAATGTCATTTTGGTGGCAGTATTTTAACTGCA 2280
 Db 2221 ATATGGCTCAGTCTACATTTTAAATTTGAAATGTCATTTTGGTGGCAGTATTTTAACTGCA 2280

QY 2281 TAATAGCCTAAACATGATTAATTTGAACCTATTATTTACACATAGTTTGAAGAAAAAGACAAA 2340
 DB TAATAGCCTAAACATGATTAATTTGAACCTATTATTTACACATAGTTTGAAGAAAAAGACAAA 2340
 QY 2341 AATAGTATTTCAGGTGAGCAATAGATTAGTATTTCCAGCTGCTACTATTTATTTTAA 2400
 DB AATAGTATTTCAGGTGAGCAATAGATTAGTATTTCCAGCTGCTACTATTTATTTTAA 2400
 QY 2401 ACACAAATCTTAAAGCTACACAAATACATACAGGCCCTTTAAAGCAGAGCTGTATGACACA 2460
 DB ACACAAATCTTAAAGCTACACAAATACATACAGGCCCTTTAAAGCAGAGCTGTATGACACA 2460
 QY 2461 TTTGGCAGTTTAAATAGATGTTACTCAAGAAATTTTAAAGAACTGATTTATTTTAA 2520
 DB TTTGGCAGTTTAAATAGATGTTACTCAAGAAATTTTAAAGAACTGATTTATTTTAA 2520
 -QY 2521 ATGGTGTTTATACAGGAGCTTGAACATGTTTGTATGATTAATTTCAAAAGTAATGC 2580
 -Jb 2521 ATGGTGTTTATACAGGAGCTTGAACATGTTTGTATGATTAATTTCAAAAGTAATGC 2580
 QY 2581 TTCAATCAGATAGTCTTTTTCACAAAGTTCAATACCTGTTTTCATGTAATTTTGTATGA 2640
 DB TTCAATCAGATAGTCTTTTTCACAAAGTTCAATACCTGTTTTCATGTAATTTTGTATGA 2640
 QY 2641 AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGCTATTAATCTGCTGAGACTT 2700
 DB AAAATCAATGTCAAGTACCAAAATGTTAATGTATGTGCTATTAATCTGCTGAGACTT 2700
 QY 2701 TCAGTGCAGTGTATAGAGTCTTAAACACACACCTTAAGAGAAAGATCGAATTTTTCAG 2760
 DB TCAGTGCAGTGTATAGAGTCTTAAACACACACCTTAAGAGAAAGATCGAATTTTTCAG 2760
 QY 2761 ATGATTCGGAATTTTCATTCAGGATTTGTAATAGTGACATATATATATATACATAT 2820
 DB ATGATTCGGAATTTTCATTCAGGATTTGTAATAGTGACATATATATATATATACATAT 2820
 QY 2821 CACCTCCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTATCA 2880
 DB CACCTCCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTATCA 2880
 QY 2881 TTCCCTTTTCCATATAGGAACATAATTTGAAGTGGCCAGATGATTTATCATGTCACT 2940
 DB TTCCCTTTTCCATATAGGAACATAATTTGAAGTGGCCAGATGATTTATCATGTCACT 2940
 QY 2941 GAAAAATTAATACCAAAATGCCACAGTAACCTTAACGATTTCTTCACCTTCTGGGGTTT 3000
 -b GAAAAATTAATACCAAAATGCCACAGTAACCTTAACGATTTCTTCACCTTCTGGGGTTT 3000
 QY 3001 TCAGTATGAACCTTAACCTCCCAACCAACATCTCCCTCCACATGTCACCAATTTCAAG 3060
 DB TCAGTATGAACCTTAACCTCCCAACCAACATCTCCCTCCACATGTCACCAATTTCAAG 3060
 QY 3061 GGCCACAGTACCTTTGCTGGGCAATTTTCCAGATGTTTACAGAGCTGTGAGTACAGCAG 3120
 DB GGCCACAGTACCTTTGCTGGGCAATTTTCCAGATGTTTACAGAGCTGTGAGTACAGCAG 3120
 QY 3121 AAAATCTTTTACTAGTGTGTGTATATATATATAAACAATTTGTAATTTCTTTAGCCC 3180
 DB AAAATCTTTTACTAGTGTGTGTATATATATATAAACAATTTGTAATTTCTTTAGCCC 3180
 QY 3181 ATTTTCTAGACTGCTCTGTGGAATATATTTGTGTGTGTATATATCATGTGTGTAT 3240
 DB ATTTTCTAGACTGCTCTGTGGAATATATTTGTGTGTGTATATATCATGTGTGTAT 3240
 QY 3241 GGTATGTATGATTTAAATCTAATCTAATTTGTCCCGGAGTTGTGCCAAAGTGCATA 3300
 DB GGTATGTATGATTTAAATCTAATCTAATTTGTCCCGGAGTTGTGCCAAAGTGCATA 3300
 QY 3301 GTCTGAGCTAAATCTAGGTGATTTGTCATCATGACAACTGCTGCTCAGTCCATTTTAAAC 3360
 DB GTCTGAGCTAAATCTAGGTGATTTGTCATCATGACAACTGCTGCTCAGTCCATTTTAAAC 3360

QY 3361 TGTAGCAACCTTCTGCAATTCATTAATCTTCTAATCATGTTTACCATTTCAAAATGGATATA 3420
 DB TGTAGCAACCTTCTGCAATTCATTAATCTTCTAATCATGTTTACCATTTCAAAATGGATATA 3420
 QY 3421 AGAGGCAAGCTGGAAGCAGATGAGCTGTGAGTACAGCAATATAGGGTTTGTGGTGGT 3480
 DB AGAGGCAAGCTGGAAGCAGATGAGCTGTGAGTACAGCAATATAGGGTTTGTGGTGGT 3480
 QY 3481 TGGTTTGATAAAGCAGTATTTGGGGTCATATTTGTTTCTGCTGTGGAGCAAAAGCTCATA 3540
 DB TGGTTTGATAAAGCAGTATTTGGGGTCATATTTGTTTCTGCTGTGGAGCAAAAGCTCATA 3540
 QY 3541 CACTTTGAAGTATTAATTTCTTATCTCAATTTCAATTTGATGATGAAATTTCCAGGT 3600
 DB CACTTTGAAGTATTAATTTCTTATCTCAATTTCAATTTGATGATGAAATTTCCAGGT 3600
 QY 3601 TGCTCATATTTCTTTCAGACTTTCGCGACAGATGCTGCTGATATAAATTAGGTAAGATA 3660
 DB TGCTCATATTTCTTTCAGACTTTCGCGACAGATGCTGCTGATATAAATTAGGTAAGATA 3660
 QY 3661 ATTTGTTGGGCCATATTTTAGGACAGTAAATAAATCAATCAGGTTCCAGTTGCTTGAATG 3720
 DB ATTTGTTGGGCCATATTTTAGGACAGTAAATAAATCAATCAGGTTCCAGTTGCTTGAATG 3720
 QY 3721 CAAGGCTAAGAGTACTGCGCTTTTGTGTAGCAGTCAAAATCTATTATTTCCACTGGCG 3780
 DB CAAGGCTAAGAGTACTGCGCTTTTGTGTAGCAGTCAAAATCTATTATTTCCACTGGCG 3780
 QY 3781 CATCATATGCAGTGATATATGCTTAAATAAGCCATAGGTTTACACCAATTTTGTAG 3840
 DB CATCATATGCAGTGATATATGCTTAAATAAGCCATAGGTTTACACCAATTTTGTAG 3840
 QY 3841 ACAATTTGCTTTTTCAGATGCTTTGTTCTTTCATATGAAAAAATGCAATTTTATA 3900
 DB ACAATTTGCTTTTTCAGATGCTTTGTTCTTTCATATGAAAAAATGCAATTTTATA 3900
 QY 3901 ATTCAAGAGTCTATAGATTTCTGAAGCGTCAACGTCGATTTTATTTATGACTGGAAG 3960
 DB ATTCAAGAGTCTATAGATTTCTGAAGCGTCAACGTCGATTTTATTTATGACTGGAAG 3960
 QY 3961 TAACTGTGTTTACTAGCAGGATATTTTCAATTTTCTACCTTTTACTACATCTTTTCAACA 4020
 DB TAACTGTGTTTACTAGCAGGATATTTTCAATTTTCTACCTTTTACTACATCTTTTCAACA 4020
 QY 4021 AGTAACCTTTGTAGAAATGAGCCAGAGCCCAAGCCCTGAGTTGGCAGTGGCCCAATAGTG 4080
 DB AGTAACCTTTGTAGAAATGAGCCAGAGCCCAAGCCCTGAGTTGGCAGTGGCCCAATAGTG 4080
 QY 4081 TAAATATAAAGTTTACAGAAACCTT 4105
 DB TAAATATAAAGTTTACAGAAACCTT 4105

RESULT 2

US-09-919-497-12
 ; Sequence 12, Application US/09919497
 ; Patent No. US20020106662A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mutter, George L.
 ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 ; FILE REFERENCE: B0801/7225
 ; CURRENT APPLICATION NUMBER: US/09/919,497
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 60/221,735
 ; PRIOR FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 2595
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-919-497-12

Query Match	60.28;	Score 2470;	DB 10;	Length 2595;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2481;	Conservative	0;	Mismatches	0;
	Indels	1;	Gaps	
QY	1624	CCAGTCATGCTCTGCTGCTCTTACCAGTCCAAAAGTCTGATGACCTCGTGCCCAT	1683	
DB	15	CCAGTCATGCTCTGCTGCTCTTACCAGTCCAAAAGTCTGATGACCTCGTGCCCAT	74	
QY	1684	GAACGGAAACGATCCAGTGGAAAGAACCCAGCATCAAAACCAACACACAGACCGGAG	1743	
DB	75	GAACGGAAACGATCCAGTGGAAAGAACCCAGCATCAAAACCAACACACAGACCGGAG	134	
QY	1744	CAGGCATAAGGACAGCATGAACTGACCAACCCCTTAAAGCACTCCTCGTACTCCCAATAA	1803	
DB	135	CAGGCATAAGGACAGCATGAACTGACCAACCCCTTAAAGCACTCCTCGTACTCCCAATAA	194	
QY	1804	CCTCTCGGAGAAAAATACAAAGCAACTGTGACTCCGGGAATCTCTCTGATCCTT	1863	
DB	195	CCTCTCGGAGAAAAATACAAAGCAACTGTGACTCCGGGAATCTCTCTGATCCTT	255	
QY	1864	CTTCTTAATTACTCCACACCCCAAGAAATGCTTCCAAACCGCAAGGTAGACTG	1923	
DB	255	CTTCTTAATTACTCCACACCCCAAGAAATGCTTCCAAACCGCAAGGTAGACTG	314	
QY	1924	GTTATCCACCCACACATCTAGCAATCGTACTCTTAAATGATCTAAATTTACATATTC	1983	
DB	315	GTTATCCACCCACACATCTAGCAATCGTACTCTTAAATGATCTAAATTTACATATTC	374	
QY	1984	TGGTCTTGTATTCAGCACTAAAAATGGTGGAGCTGGGGAGATGAAGACTGTTAAA	2043	
DB	375	TGGTCTTGTATTCAGCACTAAAAATGGTGGAGCTGGGGAGATGAAGACTGTTAAA	434	
- QY	2044	TGAACACAGAAGGATATTACTACTTTTGCATCAAAATAGAGCTTTCAGTACATGGCTA	2103	
DB	435	TGAACACAGAAGGATATTACTACTTTTGCATCAAAATAGAGCTTTCAGTACATGGCTA	494	
QY	2104	GCTTTTATGGCAGTCTGGTGAATGTCAATGGGAATGGTCAACCTGAACTTTAGAGA	2163	
- DB	495	GCTTTTATGGCAGTCTGGTGAATGTCAATGGGAATGGTCAACCTGAACTTTAGAGA	554	
QY	2164	TTAACGACAAGATTTTCTACTTTTTTAAAGTGATTTTTTGTCTTCAGCCAAACAATA	2223	
DB	555	TTAACGACAAGATTTTCTACTTTTTTAAAGTGATTTTTTGTCTTCAGCCAAACAATA	614	
QY	2224	TGGGCTCAGGTCACCTTTTATTTGAAATGTCAATGGTGGCAGTATTTTTTAACTGCATAA	2283	
DB	615	TGGGCTCAGGTCACCTTTTATTTGAAATGTCAATGGTGGCAGTATTTTTTAACTGCATAA	674	
QY	2284	TAGCCTAACATGATTTTGAACCTATTTTACACATAGTTTGAAGAAAAAAGACAAAAAT	2343	
-	675	TAGCCTAACATGATTTTGAACCTATTTTACACATAGTTTGAAGAAAAAAGACAAAAAT	734	
QY	2344	AGTATTCAGGTCAGCAATTTAGATTTTCCAGCTCACATTTATTTTTTAAAAACA	2403	
DB	735	AGTATTCAGGTCAGCAATTTAGATTTTCCAGCTCACATTTATTTTTTAAAAACA	794	
QY	2404	CAAAATCTAAAGCTACACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463	
DB	795	CAAAATCTAAAGCTACACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854	
QY	2464	GGCAGTTTAAATAGTGTACTCAAGAAATTTTTTAAAGCACTGATTTTTTAAATG	2523	
DB	855	GGCAGTTTAAATAGTGTACTCAAGAAATTTTTTAAAGCACTGATTTTTTAAATG	914	
QY	2524	GTGTTTTTATACAAGGGACCTTGAACATGTTTGTATGTTAAATTCAAAAGTAATGCTTC	2583	
DB	915	GTGTTTTTATACAAGGGACCTTGAACATGTTTGTATGTTAAATTCAAAAGTAATGCTTC	974	
QY	2584	AATCAGATAGTTCCTTTTTCAAAAGTTCAATACTGTTTTTTCATGTAATTTTGTATGAATA	2643	
DB	975	AATCAGATAGTTCCTTTTTCAAAAGTTCAATACTGTTTTTTCATGTAATTTTGTATGAATA	1033	
QY	2644	ATCAATGTCAAGTACCAAAATGTTAACTATGTGTCAATTAACCTGCTGAGACTTTCA	2703	

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Db 2114 GGCTAAGAACTACTGCCCTTTTGTGTTAGCAGTCAAAATCTATTATTCACCTGGCCAT 2173
QY 3784 CATATGCCAGTATATATGCTTATAATATAGCCATAGGTTACACCATTTTGTATTAGACA 3843
Db 2174 CATATGCCAGTATATATGCTTATAATATAGCCATAGGTTACACCATTTTGTATTAGACA 2233
QY 3844 ATTGCTTTTTCAGATGCTTTGTTCTTTTCATATGAAATAATGCAATTTTATAAAT 3903
Db 2234 ATTGCTTTTTCAGATGCTTTGTTCTTTTCATATGAAATAATGCAATTTTATAAAT 2293
QY 3904 CAGAAAGTCATAGATTCTGAAGGCTCAACGTGCACTTTTATTATGGAAGTGAAGTAA 3963
Db 2294 CAGAAAGTCATAGATTCTGAAGGCTCAACGTGCACTTTTATTATGGAAGTGAAGTAA 2353
QY 3964 CTGTGTTTACTAGCAGGAATATTTCCAAATTTCTACTTTTACTACATCTTTTCAACAAGT 4023
Db 2354 CTGTGTTTACTAGCAGGAATATTTCCAAATTTCTACTTTTACTACATCTTTTCAACAAGT 2413
Y 4024 AACTTTGTAGAAATGAGCCAGAGCCAGGCGCTGAGTTGGCAGTGGCCCAATAAGTAA 4083
Db 2414 AACTTTGTAGAAATGAGCCAGAGCCAGGCGCTGAGTTGGCAGTGGCCCAATAAGTAA 2473
QY 4084 AATAAAAGTTTACAGAAACCTT 4105
Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 3
US-09-931-157-2
; Sequence 2, Application US/09931157
; Patent No. US200200824141
; GENERAL INFORMATION:
; APPLICANT: Imura, Hiroo
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4301
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)...(1566)
US-09-931-157-2

Query Match 9.6%; Score 395.8; DB 10; Length 4301;
Best Local Similarity 65.7%; Pred. No. 6.8e-84;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

QY 689 TGCCACAGCAGACGATAAATTTACTTTCAGCTTTCAAAATACATTAACACTGTGATATCTGT 748
Db 505 TGCCAGAGCCATCGAGATCAAGAGACTTTCAAAATACATCAACACGGTTGTGCTCGC 564
QY 749 ACTATTTTCATCGTGGGAATGTTGGGGAATGCACTCTGCTCAGGATCATTTTACCAGAAC 808
Db 565 CTGTGTTTCGTCGGGATCATCGGAACCTCCACACTCTCAGAAATATCTACAGAAC 624
QY 809 AAATGTATGAGAAATGGCCCAACGCGTGTAGCCAGCTTTGCCCTTGGAGACCTTATC 868
Db 625 AAGTGCATGCGAAACGGTCCCAATATCTTGTATCGCCAGCTTGGCTCTGGAGACCTGCTG 684
QY 869 TATGTGGTCATGTCCTCCCTCATCAATGATTTAAGTGTGCTGGCTGGCGCTGGCCCTTTT 928
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Db 685 CACATCGTCATTTGACATCCCTATCAATGTCTACAAGCTGTGCGAGAGAGCTGCC----- 740
QY 929 GATCACAAATGACTTTGGCGTATTTTGAAGCTGTTCCCTTTTTCGACAGAGTCCCTCG 988
Db 741 -----ATTGGAGCTGAGATGTGAAGCTGGTCTTTTCATACAGAAAGCCTCC 789
QY 989 GTGGGATCACCCCTCCCTCAACCTCTGCGCTCTAGTCTTGACAGGTACAGAGCAGTTGCC 1048
Db 790 GTGGGATCACTGCTGAGTCTATGTGCTCTGAGTATTCACAGATATCGAGCTGTGCT 849
QY 1049 TCTGTGAGTCTGCTTTCAGGGAATTTGGGATTTCTTGTGAATGCCATTTGAAATTTGCTCC 1108
Db 850 TCTTGGAGTAGAATTAAGGAATTTGGGTTCCAAATTTGACAGCAGTAGAATTTGTTTTG 909
QY 1109 ATCTGATCTGCTCCCTTATCTCTGGCCATTTCTTGAAGCGATTTGGCTTCGTCATGGTACC 1168
Db 910 ATTTGGTGGTCTCTGCTGTTCTTGGCTTCCCTGAAGCCATAGGTTTGTATATAATTTACG 969
QY 1169 TTTGAATATAGGGGTGAACAGCATATAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
Db 970 ATGGACTACAAGGAAGTTATCTGCGAATCTGCTTGTTCATCCCTTCAGAGACAGCT 1029
QY 1223 TTCATGGAGTTTACCAAGATGTAAGGACTGTTGGCTCTTTCGGGTTCTATTTCTGTATG 1282
Db 1030 TTCATGCACTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTCTATTTCTGCTTG 1089
QY 1283 CCCTTGGTGTGCACTCGGATCTTCTACCCCTCATGCTTGTGAGATGTTGAACAGAGG 1342
Db 1090 CCATTTGGCCATCACTGCTCATTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146
QY 1343 AATGGCAGCTTGAGAAATGCGCTCAGTGAACATCTTAAGCAGCGTCGAGAGTGGCAAAA 1402
Db 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAGCAGAGACGGGAAGTGGCCAAA 1206
QY 1403 ACAGTTTCTGCTGCTGTTGTTGTTTCTTCTTCTGTTGTTGTTCTTCTTCTTCTTCTTCTTCT 1462
Db 1207 ACCGCTTTTGGCTGCTGCTGCTGCTGCTTGTGCTTGTGCTGCTTGTGCTTGTGCTGCTGCTG 1266
QY 1463 ATATTGAAGAAACTGTGTATAACGAAATGGCAAGAACCGATGTGAATTTACTTAGTTTC 1522
Db 1267 ATTTCTGAAGCTCACCTCTTTTATAATCAAGATGATCCCAATAGATGTGAACCTTTT 1326
QY 1523 TTACTGCTCATGGATACATCGGTATTAATTAATTTGGGCAACCAATGAATTCATGATATAA 1582
Db 1327 CTGTTGGTATTTGGACTATATGTTGATCAACATGGCTTCACTGAATTTCTGCTTAAACCCA 1386
QY 1583 ATAGCTCTGATTTTGTGAGCAAGAAATTTAAAAATTTGTTTCCAGTCATCCCTCTGCTGC 1642
Db 1387 ATGCTCTGATTTTGGTGAAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGC 1446
QY 1643 TGCTG 1647
Db 1447 TGGTG 1451
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RESULT 4
US-09-867-701-3320
; Sequence 3320, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3320
; LENGTH: 438
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i ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(438)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-3320

Query Match 6.9%; Score 284.4; DB 10; Length 438;
Best Local Similarity 89.1%; Pred. No. 4.9e-58;
Matches 383; Conservative 0; Mismatches 34; Indels 13; Gaps 7;

QY 1577 AACCCCATAGCTCTGATTTTGTGAGCAAGAAATTTAAATTTGTTCCAGTCATGCCCTC 1636
Db 9 AACCCCATAGCTCTGATTTTGTGAGCAAGAAATTTAAATTTGTTCCAGTCATGCCCTC 68

QY 1637 TGCCTGCTCTGTACCACTGCCAAAGTCTGTAGCTCGGTCCCATGAACGGAACAAGC 1696
Db 69 TNCCTGCTCTGTACCACTGCCAAAGTCTGTAGCTCGGTCCCATGAACGGAACAAGC 128

QY 1697 ATCCAGTGAAGAACCCAGCATCAAAACCAACCAACACAGACCGGAGGAGCCATAAGGAC 1756
Db 129 ATCCAGTGAAGAACCCAGCATCAAAACCAACCAACACAGACCGGAGGAGCCATAAGGAC 188

QY 1757 AGCATGAACACACACCCCTTAGAGCACTCTCGGTACTCCCATTAATCCTCTCGGA-GAA 1815
Db 189 AGCATGAACACACACCCCTTAGAGCACTCTCGGTACTCCCATTAATCCTCTCGGA-GAA 248

QY 1816 AAAATACAAAGGAACACTGCA--CTCCGGGAATCTCTCTCTGAT--CCTCTCTCCCTTA 1871
Db 249 AAAATACAAAGGAACACTGCAAGTCCGGGAATCTNTCTCTGCTCTCTCTCTCTCTGA 308

QY 1872 ATTCACCTCCCAACCCCAAGAA--GAAATGCTTTCCAAACCGCAAGTAG--ACTGGTT 1926
Db 309 ATTCACCTCCCAACCCCAAGGAATGTTTCCAAACCGGAAGGTGGACTGGTTT 368

QY 1927 TATCCACCAACAACA-TCTACGAATCGTACTCTCTTT--AATGAFCTAATTTACATATTC 1983
Db 369 TTTCCACCAACAACAATTTAGGATTCGTACTCTTTCTTTAATTTGGTTCTAATTTACATATTC 428

QY 1984 TGCCTGTGTGT 1993
Db 429 TGCCTGTGTGT 438

RESULT 5
US-09-954-531-917/c
; Sequence 917, Application US/09954531
; Patent No. US20020165180A1
--GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cando
; FILE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 917
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1)...(592)
; OTHER INFORMATION: n=a,t,g or c
US-09-954-531-917

Query Match 3.6%; Score 147; DB 9; Length 592;
Best Local Similarity 65.4%; Pred. No. 2.4e-25;
Matches 229; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 1301 ATCTTCTACACCCCTCATGACTTGTGAGATGTTGAACAGAGGAATGGCAGCTTGAGAAAT 1360
Db 468 ATTTTATACACTAANGACCTGTGAAATGTTGAGAAGGAAAGTGGCATGCGAGATTGCT 409

QY 1361 GCCCTCAGTGAACATCTTAAGCAGCGTTCGAGAAAGTGC---AAAAACAGTTTTCTGCTTG 1417
Db 408 TTAATGAGCACCCTTAAGCCAGAGCCGGAAGTGGCCCAAAANCCGGTCTTTTGGCTG 349

QY 1418 GTTGAATTTTGTCTTTTGGTTCCTCTTCACTTAAGCCGTATATTAAGAAAAACT 1477
Db 348 GTCTGGTCTTTTGGCTCTGCTGGCTTCCCTTCACTCAGCAGGATTCTGAAGCTCACT 289

QY 1478 GTGTATACGAATGGACAAGAACCGATGTGAATTTACTTTAGTTTCTTACTGCTCATGGAT 1537
Db 288 CTTTATAATCAGATGATCCCAATAGATGTGAATTTTGGCTTTCTGTTGGTATTGGAC 229

QY 1538 TACATCGGTATTAACTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTGTATTTT 1597
Db 228 TATATTGGTATCAACATGCTTCACTGAATTCCTGCAATTAACCAATGCTCTGTATTG 169

QY 1598 GTGAGCAAGAAATTTAAATTTGTTTCCAGTCATGCTCTGCTGTGCTG 1647
Db 168 GTGAGCAAGAAATTTCAAAACCTGCTTAAAGTCATGCTTATGCTGTGCTG 119

RESULT 6
US-09-962-436-531/c
; Sequence 531, Application US/09962436
; Patent No. US20020081301A1
--GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 531
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-962-436-531

Query Match 3.6%; Score 147; DB 10; Length 592;
Best Local Similarity 65.4%; Pred. No. 2.4e-25;
Matches 229; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 1301 ATCTTCTACACCCCTCATGACTTGTGAGATGTTGAACAGAGGAATGGCAGCTTGAGAAAT 1360
Db 468 ATTTTATACACTAANGACCTGTGAAATGTTGAGAAGGAAAGTGGCATGCGAGATTGCT 409

QY 1361 GCCCTCAGTGAACATCTTAAGCAGCGTTCGAGAAAGTGC---AAAAACAGTTTTCTGCTTG 1417
Db 408 TTAATGAGCACCCTTAAGCCAGAGCCGGAAGTGGCCCAAAANCCGGTCTTTTGGCTG 349

QY 1418 GTTGAATTTTGTCTTTTGGTTCCTCTTCACTTAAGCCGTATATTAAGAAAAACT 1477
```


Db 348 GTCTGGTCTTTGGCCCTCTGCTGGCTTCCCTTCACTCAGCAGGATTCTGAAGCTCACT 289
QY 1478 GTGTATACGAAGTAAAGCAAGCAGATGTGAATTTACTTAGTTCTTACTGCTCATGGAT 1537
Db 288 CTTTATATCAGATGATCCCAATAGATGTGAATTTTGAGCTTTCTGTGGTATTTGGAC 229
QY 1538 TACATCGGTATTAATCTGGCAACCATGAATTCATGTATATAACCCCATGCTCTGTATTTT 1597
Db 228 TATATTTGTATCAACATGGCTTCACTGAATTCCTGCAATTAACCCCAATGCTCTGTATTTG 169
QY 1598 GTGACGAGAAATTTAAATTTGTTCCAGTCATGCTCTGCTGCTGCTG 1647
Db 168 GTGACCAAGAAATTCAAAATGCTTTAAGTCATGCTTATGCTGCTGCTG 119

RESULT 7
US-09-880-107-2060/c
Sequence 2060, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherif, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2060
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(592)
OTHER INFORMATION: n = a or c or g or t

US-09-880-107-2060
Query Match 3.6%; Score 147; DB 10; Length 592;
Best Local Similarity 65.4%; Pred. No. 2.4e-25;
Matches 229; Conservative 0; Mismatches 118; Indels 3; Gaps 1;
QY 1301 ATCTTCTACACCCCTCATGACTTGTGAGATGTTGAACAGAAAGATGGCAGCTTGAGAAAT 1360
Db 468 ATTTTATACACTTAAGACACCTGTGAATGTTGAAGAGAAAGTGGCATGCAGATTGCT 409
QY 1361 GCCCTCAGTGAACATCTTAAGCAGCTGCGAAGTGGC---AAAACAGATTTTCTGCTTG 1417
Db 408 TTAATAGACACCCCTTAAGCAGCAGCGGNAAGTGGCCCAAAANCCGGCTTTTGGCCTG 349
QY 1418 GTTGTAATTTTGTCTTGTGTTCCCTCTTCACTTAAGCCGATATATTGAAGAAACT 1477
Db 348 GTCTGGTCTTTGGCCCTCTGCTGGCTTCCCTTCACTCAGCAGGATTTCTGAAGCTCACT 289
QY 1478 GTGTATACGAAGTAAAGCAAGCAGATGTGAATTTACTTAGTTCTTACTGCTCATGGAT 1537
Db 288 CTTTATATCAGATGATCCCAATAGATGTGAATTTTGAGCTTTCTCTGTTGATTTGGAC 229
QY 1538 TACATCGGTATTAATCTGGCAACCATGAATTCATGTATATAACCCCATGCTCTGTATTTT 1597
Db 228 TATATTTGTATCAACATGGCTTCACTGAATTCCTGCAATTAACCCCAATGCTCTGTATTTG 169
QY 1598 GTGACGAGAAATTTAAATTTGTTCCAGTCATGCTCTGCTGCTGCTG 1647
Db 168 GTGACCAAGAAATTCAAAATGCTTTAAGTCATGCTTATGCTGCTGCTG 119

RESULT 8

US-09-778-927A-27
Sequence 27, Application US/09778927A
Patent No. US20020068342A1
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: IL 134453
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL135341
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 800
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(800)
OTHER INFORMATION: n = a,c,g,t any unknown or other

US-09-778-927A-27
Query Match 2.8%; Score 114.6; DB 10; Length 800;
Best Local Similarity 67.2%; Pred. No. 1.4e-17;
Matches 162; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 689 TGCCACAGCAGACATAAAATTTACTTCAGCTTTCAAAATACATTAACACTGTGATATCTTGT 748
Db 505 TGCCAGGACCCATCGAGATCAAGGAGACTTTCAATACATCAACACGGTTGTGCTCTGC 564
QY 749 ACTATTTTCATCGTGGGAATGGTGGGAATGCAACTCTGCTCAGGATCAATTTACCAGAAC 808
Db 565 CTGTGTCTGCTGGGATCATCGGGAACCTCCCAATATCTTGATCGCCAGCTTGGCTCTGGAGACCTGCTG 684
QY 809 AAATCTATGAGGAATGGCCCAACGCGCTGATAGCCAGCTTGGCCCTTGAGACCTTATC 868
Db 625 AAGTCATCGGAACGCGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGAGACCTGCTG 684
QY 869 TATGTGTCATGATCTCCCTATCAATGATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928
Db 685 CACATCGTCATTTGACATCCCTATCAATGCTACAAAGCTGCTGCAGGAGACTGGCCATT 744
QY 929 G 929
Db 745 G 745

RESULT 9

US-09-160-116-11
Sequence 11, Application US/09160116A
Patent No. US20010014457A1
GENERAL INFORMATION:
APPLICANT: Spindel, Elliot R.
APPLICANT: Barry, Brenda
APPLICANT: Negalla, Srinivasa
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
FILE REFERENCE: 00537/098003
CURRENT APPLICATION NUMBER: US/09/160,116A
CURRENT FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: US 08/910,098
PRIOR FILING DATE: 1997-08-12
PRIOR APPLICATION NUMBER: US 08/279,590
PRIOR FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11

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; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(1198)
US-09-160-116-11

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Query Match      1.7%; Score 68.4; DB 10; Length 2595;
Best Local Similarity 46.1%; Pred. No. 2.6e-06;
Matches 412; Conservative 0; Mismatches 446; Indels 36; Gaps 4;

QY 761 GTGGGAATGTTGGGGAATGCAACTCTGCTCAGGATGATTTACACAGACAATGATGAGG 820
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 GTGGGATCCTCGGAATGCTATCCCTCAATCAAGACTCTTTTCAAGACTAATCCATGCAA 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 821 AATGGCCCCAACCGGTGTAGTCCAGTCTTGGCCCTTGGAGACCTTATCTATGTGGTCATT 880
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 ACAGTTCCAAATATTTTCATCACCGCTGGCTTTTGGAGATCTGTTACTCTGCTGACT 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 881 GATCTCCCTATCAATGATTTAAGTGTGCTGGCTGGGCGCTGGCCCTTTGATCACAAATGAC 940
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 TGTGTGCCAGTGGATGATCAACCCACTACCTGGCAGAGGATGGCTGTTGGAAAGGTCGG- 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 941 TTTGGCGTATTTCTTGCAGCTGTTCCCTCTTTTTCAGAGTCTCTCGGTGGGATCAC 1000
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 -----TTGTAAGTGTCTTCTTCATCCGGCTCACTTCTGCTGGTGTATCA 403
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1001 GTCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGCACTTGCCTCTGGAGTCGT 1060
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 404 GTGTTACCGCTAACAAATCTCAGCGTACAGATCAAAAGCAGTGTGAGCCACTTGAA 463
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1061 GTTCAGGGAATTTGGGATTCCTTTGTGTAAGTCCATTTGAAATTTGCTTCCATCTGGATCCTG 1120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 464 CGACAGCCCTCCAAATGCCATTTCTGAAGACCTGTGCCAAAGCTGGTGCATCTGATCATG 523
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1121 TCCTTTATCTCGGCATTTCTCAAGCGATTTGGCTGCTCATGTACCCCTTTGAATATAGG 1180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 524 GCTATGATTTTGTCTGTGCGAGGCTATTTCTCAAAATGTATACACTTTTCCAAGATCCT 583
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1181 GGTGAACAGCATAAACCTGTATGTCTCAATGCCACATCAAAATTCATGAGTTCTACCAA 1240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 584 AACAGAAAGTAAACATTTGAATCCCTGTAATCTCTACCCCTATCTCTGAGAGGCTTTTGAC 643
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1241 GATGTAAGGACTGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTGGTGTGCACTGGG 1300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 644 GAAATACATTTCTCTGTGTGTTTCTTGTGTTCTTACATTATCCCGCTCTCGATTATCTCT 703
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1301 ATCTTCTACCCCTCATGACTTGTGAGATGTTGAACAGAGGAATGGGAGCTTGAGAAT 1360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 704 GTCATATTATCTTGTATGCCAGGACTCTTTTACAAAGCACCTTGAACATACCGACTGAG 763
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1361 GCCCTCAGTGAACATCTTAAAGCAGGCTGCGAGA-----AGTGCAAAACAGTTTTC 1411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 764 GAACAAAGCCATGCCCGGAAGCAGATTGAATCCCGGAAGAGAAATGCCAAACGGTACTG 823
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1412 TCGTTGGTTGTAATTTTGTCTCTTTGCTGGTTTCCCTCTTCTTCACTTAAGCCGATATAGAG 1471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 824 GTGCTGGTGGCTCTGTGCGCACTCTGCTGGTTGCGGAATCACT--CCTGTATCTCTATC 881
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1472 AAAACTGTGTATAAGAAATGGACAAGAACCGATGTGAATTAATTAATTAATTAATTAAT 1531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 882 ACTCAATCACTTATGAAGAGTACGAGAGCCCTTCTGATGTCCCTTTGCTGTCACCAAT 940
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1532 ATGGATTACATCGGTATTAACTTTGGCAACCATGAATTCATGATATAAACCCTACTCTG 1591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 941 -----TTCTCTCGGGTGTGCTTTTCAAGTAATCTCGGTGAACCCCTTGTCTG 991
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1592 TATTTTGTGAGCAAAATTTAAATATTTTCCAGTCACTGCTCTGCTGCTGTC 1645
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 992 TATTGGCTGAGCAAGACCTTCCAGAGCATTTTAAAGGCTCAGCTCTGCTGCTTC 1045
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 10
US-09-160-116-1
; Sequence 1, Application US/09160116A
; Patent No. US20010014457A1
; GENERAL INFORMATION:
; APPLICANT: Spindel, Elliot R.
; APPLICANT: Negalla, Srinivasa
; APPLICANT: Barry, Brenda
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
; FILE REFERENCE: 00537/098003
; CURRENT APPLICATION NUMBER: US/09/160,116A
; CURRENT FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 08/910,098
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: US 08/279,590
; PRIOR FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1563
; TYPE: DNA
; ORGANISM: Bombina bombina
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)...(1319)
US-09-160-116-1

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Query Match      1.5%; Score 62; DB 10; Length 1563;
Best Local Similarity 45.3%; Pred. No. 6.4e-05;
Matches 331; Conservative 0; Mismatches 375; Indels 24; Gaps 2;

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QY 735 CTGTGATATCTTCTGATATTTTTCATCTGTTGGAATGTTGGGAATGCAACTCTGCTCAGGA 794
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 340 CTGTACATATGCTGTATTTTCTGTCGGTATCTTGGAAACACAATACTTATAAAG 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 795 TCATTTACCAGAAACAAATGATGAGGAATGGCCCAACGCGTGATAGCAGCTTTGCC 854
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 TATTTTAAAAATCAAGTCAATGCAGACTGTTCTTAATATTTTCATCAACCAGCTGCTT 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 855 TTGGAGACCTTATCTATGTTGGTCAATGATCTCCCTCATGATGATTTTAACTGCTGCTG 914
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 460 TTGGAGATCTTCTTCTTACTGCTGACCTGGCTGCCAGTGGACGATCTCGGTATATTGTGG 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 915 GCGCTGTGGCTTTTGTATCAATGACTTTTGGCGTATTTTCTTTCGAAAGCTTCCCTCTTT 974
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 ACAGCTGGATGTTTGGAGAGCTGGCTGT-----AGATAATTTCTCTCA 564
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 975 TCGAGAAGTCTCGGTGGGAGTACCGCTCTCAACCTCTGCGCTCTTAGTGTGACAGGT 1034
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 565 TACAGCTTACCTCTGTCGGAGTGTGCTGTTTACTTTTAACTGTCTCAGTACTGACAGGT 624
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1035 ACAGAGCACTTGCCTCTGAGTGTGTTTCAGGAATTTGGGATTCCTTTGGTAACCTGCCA 1094
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 625 ACAGAGCACTTGTGAACCCCTTGCATCTGCACTGACATGCGCTTTTGAAGACATGTG 684
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1095 TTGAATTTCTCCATCTGATCTCTCTTCTTCTTCTGCGCATCTCTGAGCGATTTGGCT 1154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 685 GCAAGCTGTTTGTGTTTGGATCAITTCATCTCTCTGCTGCTCCAGAGCTGTGTTCT 744
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1155 TCGTATGTCACCTTTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCCA 1214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 745 CAGATTTGTATGAATTTGGCAGCTCGGAAAAAATACCACCTTTTGAAGCCTGTGCTCCAT 804
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1215 CATCAAAATTCATGAGTCTTACCAGATGTAAGGACTGGTGGCTCTTCGGGTCTTATT 1274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 805 ATCCAGTCTCTGAAAGATTTCTGCAAGACACATTTCCCTAATATGCTTCTCTGTTCT 864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1275 TCTGTATGCCCTTGTGTGCTGCTGCTCTTCTTACACCTCTCATGACTTGTGAGATCTGA 1334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 865 ACATTGTTCCCTGTCAATCATTTCTGATATTTCTTCTTATTTGCAAAACCCCTGTACA 924
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1335 A-----CAGAGGAATGGCAGCTTGAGAAATTCCTCAGTGAACATCTTAAGCAGC 1385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Dd  925  AAAGTACTTTTCACATGCCTGCTGAAGAGCACACTCAGCGCCGAGAAAACAGATACGCG 984
Qy  1386  GTCGAGAGTGGCAAAAACAGTTTTTCGCTGGTGTGTAATTTTGTCTCTTTGCTGGTTC 1445
Dd  985  GCAAACGAGTGGCAAAAACAGTGTGCTTGTGGGGCGCTATTGTGCTGTCTGTGGGCTCC 1044
Qy  1446  CTCCTTCACCT 1455
Dd  1045  CTAACCCACAT 1054

RESULT 11
US-09-960-352-4584
; Sequence 4584, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960, 352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4584
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB3057-016-Q1-K1-E11
US-09-960-352-4584

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Query Match	1.3%	Score 54	DB 10	Length 416	
Best Local Similarity	45.8%	Pred. No. 0.0023			
Matches 186	Conservative	0	Mismatches 220	Indels 0	Gaps 0

QY	2243	TTTCAAATGTCATTTGGTCAGATATTTTAACTGCATAATAGCCCTAACATGATTAATTT	2302
Db	1	TTGG	60
QY	2303	GAACTTATTTACACATAGTTTGGAAAAAAGACAAAAATAGTATTCAGTGAGCAATTT	2362
Db	61	TATTTTTTTTTTATTTTTTTTAAAAAAGAAAAAATTTAAATGAAAAATAGAAAAATAA	120
QY	2363	AGATTAGTATTTTCCAGCTCAGTATTTATTTTTTAAACACAAATCTCAAGCTACAAC	2422
b	121	AAAAATTAATTTTTTAAAAAAGAAAAAATAAATTTAAAAAAGAAAAAAGAAAAA	180
QY	2423	AAATACTACAGGCCCTTAAAGCACAGCTGATGACACATTTGGCAGTTTAATAGATGTTA	2482
Db	181	AAAAAGATTTTAAAAATTTAAAAATAAAAATTTAAAAAATTCATAAAAAAATAATTTA	240
QY	2483	CTCAAGAAATTTTTTGAAGACTGTATTTATTTTTTAAAGTGCTGTTTATTCAGGGAC	2542
Db	241	AAAAAAGAAATTTTTTAAATTTTTTAAAGAAAAAATTTTTTAAAAATTTTAAAAAT	300
QY	2543	CTTGAACATGTTTGTATGTTTAAATTTCAAAAGTAATGCTTCAATCAGATAGTTCTCTTTC	2602
Db	301	ATAGAAGATATAAAAAAGATTTTATTAATAATAATTTTAAAAATATATATGCGTAATTT	360
QY	2603	ACAGTTCAATACGTTTTTTCATGATAAATTTTTGTGAAAAATCAA	2648
Db	361	TATAAATTTAAAAATTTTTTAAATAAAAATTTTTTAAATTTAAAAAAGAAAAA	406

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RESULT 12
US-09-804-551B-33
; Sequence 33, Application US/09804551B
; Patent No. US20020036151A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Receptors for peptides from insects

```

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? FILE REFERENCE: Le A 34 394
? CURRENT APPLICATION NUMBER: US/09/804,551B
? CURRENT FILING DATE: 2001-03-12
? PRIOR APPLICATION NUMBER: DE 100 13 618.4
? PRIOR FILING DATE: 2000-03-18
? NUMBER OF SEQ ID NOS: 92
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 33
? LENGTH: 1521
? TYPE: DNA
? ORGANISM: Drosophila melanogaster
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(1518)
? NAME/KEY: n
? LOCATION: 1521
? OTHER INFORMATION: n is a o r g o r c o r t/
? US-09-804-551B-33

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		Query Match	1.2%; Score 50.2; DB 10;	Length 152l;	
		Best Local Similarity	48.5%;	Pred. No. 0.04;	
		Matches 216; Conservative	0;	Mismatches 208; Indels	21; Gaps
					2;
<hr/>					
Qy	725	TACATTAACTGTGATCTTGTTACTATTTTCATCGTGGGAATGGTGGGGAATGCCRACT	784		
Dd	208	TACATTGTCACTGCCTGTGTACAAGCCTCATCTTCAATTGGAGATTTTTGGCAAGCGGACG	267		
Qy	785	CTGCTCAGGATCATTTACCAGAATAATGTATAGGAATGGCCCCAACCGCCTCATAGCC	844		
Dd	268	CTGGTCATCATCTCTTTGCCACCGCTCCATGGCAAATACCCACACATATCTTT	327		
Qy	845	AGTCTTCCCCTTGGAGACCTTAATCTAATGGTGCTAATGATCTCCCTATCAATGTAATTTAAG	904		
Dd	328	TCACTGGCCCCTGGCTGATCTGTGTGTTATATGGTGTGTGTACCTGTGGCCACGATTTGTC	387		
Qy	905	CTGCTGSGCTGGGCGCTGGCCCTTTTGATCACAAATGACATTTGGCGTATTTCTTTGGCAAGCTG	964		
Dd	388	TACACGAGGAAGCTGGCCCTTTGACGGNAACA-----TGTCGGCGATC	432		
Qy	965	TTCCCTCTTTTGGCAGAAGTCCCTGGTGGGATCACCGCTCTCAACCTCTCGGCTCTTAGT	1024		
Dd	433	AGCGAGTCTTTAAGGACATATCCATCGGGGTGTCCGTGTTTACACTGACGCGCCTTTCC	492		
Qy	1025	GTTGCACAGGTPACAGACAGTGTCCCTCCTGGAGTCTGTCTCAGGGAATTTGGATTCCTTTG	1084		
Dd	493	GGCGAGCGTACTGGCCATTGTA-----AATCCCCCTACGAAGCTTCAGACCAAGCCG	546		
<hr/>					
Qy	1085	GTAACTGCCAATTGAAATTTGCTCCATCTGGATCTGTCTTATPCTTGGCCATTCTCGAA	1144		
Dd	547	CTCACTCTCTTTACTCGGGTGATGATCTTGATCTGGCATCTGGCATCTCCFACHGGCATGCCCTCG	606		

RESULT 13

RESOLV IS
US/09-960-352-6528
; Sequence 6528, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND
; TITLE OF INVENTION: MUSCLE AND FAT D
; FILE REFERENCE: 16511.006/37-21(10298
; CURRENT APPLICATION NUMBER: US/09/960
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6528
; LENGTH: 414

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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 28-LIB3058-032-Q1-K1-G11
US-09-960-352-6528

Query Match      1.2%; Score 49.6; DB 10; Length 414;
Best Local Similarity 48.6%; Pred. No. 0.026;
Matches 136; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 2359 AATTAGATTAGTATTTTCCACGCTACTATTTATTTTAAACACAAATCTTAAGCTA 2418
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Db 124 ATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTT 183

QY 2419 CAACAAATACACAGGCCCTTTAAAGCAGCTGTATGACACATTTGGCAGTTTATATAGAT 2478
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Db 184 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 243

QY 2479 GTTACTCAAGAAATTTTAAAGACTGTATTTATTTTAAAGGCTTTTATTTATACAG 2538
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 303

2539 GGACCTTGAACATGTTTGTATGTAAATTCAAAGTAATGCTTCAATCAGATAGTCTT 2598
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
304 ATATATATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTA 363

QY 2599 TTTCAAGTTCAATCTGTTTTCATGTAATTTTGTAT 2638
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 403

RESULT 14
US-09-960-352-11234
; Sequence 11234, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11234
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-052-Q1-K1-D8
09-960-352-11234

Query Match      1.2%; Score 48.6; DB 10; Length 419;
Best Local Similarity 46.8%; Pred. No. 0.045;
Matches 185; Conservative 0; Mismatches 209; Indels 1; Gaps 1;

QY 2174 GATTTCTACTTTTTTTAAAGGATTTTTTTCCTTCAGCCAAACACAAATATGGCTCAGG 2233
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Db 24 GCITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 83

QY 2234 TCACATTTTATTTGAATGTTCATTTGGGCCAGTATTTTAACTGCATAATAGCCTAACA 2293
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 143

QY 2294 TGATTTATTCGACATTTTACACATAGTTTGAAAAAAGACAAAAAATAGTATTCAGG 2353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 144 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAATAATAATAAAAAATTTTAAA 203

QY 2354 TGACCAATTAGATTAGTATTTTCACGCTCACTATTTATTTTAAACACAAATTTCTAA 2413
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 204 AGTTAAATTTATTAATTTTATTTTAAATAAAAAAATTTTTTTTATATATTTTATTTT 263

QY 2414 AGCTACAACAAATACTACAGGCCCTTAAAGCAGCTGTGATGACACATTTGGCAGTTTAA 2473
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Db 264 AATTTAAATTAATTTTAAAAATTTTAAAAATTTTAAAAATTTATATTTAA-ATAAATAATAAAT 322
QY 2474 TAGATGTTACTCAAGAATTTTAAAGAACTGTATTTTAAATGGTGTGTTTATTT 2533
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Db 323 AAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTATATATAAAT 382
QY 2534 ACAAGGACCTTGAACATGTTTGTATGTAAATTT 2568
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Db 383 AATTTTATTTTAAAAATATATATTTTAAAAATTT 417

RESULT 15
US-09-761-962-2
; Sequence 2, Application US/09761962
; Patent No. US20020077285A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: Identification and Characterization of Multiple Splice
; TITLE OF INVENTION: Variants of Mu-
; TITLE OF INVENTION: opiod Receptor (MOR-1) Gene
; FILE REFERENCE: 830002-2000.1
; CURRENT APPLICATION NUMBER: US/09/761,962
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/743,872
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-761-962-2

Query Match      1.1%; Score 46.8; DB 10; Length 1238;
Best Local Similarity 51.4%; Pred. No. 0.23;
Matches 108; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 940 CTTTGGCGTATTTCTTTCAGCTCTTCCCTTTTGGCAGAGTCTCGTGGGGATCAC 999
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 CTTTGGAAACATCCCTCTCGAGATCGTGATCTCAATAGACTACTACACATGTTCCACG 361

QY 1000 CGTCTCAACCTCTGCGCTCTTAGTGTTCACAGAGTACAGAGCAGTTGCTCTCGAGTCG 1059
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 TATCTTCACCTCTGCGCACCATGAGTGTAGACGCTACATTGCGCTGCCACCGTCAA 421

QY 1060 TGTTCAAGGAATTTGGGATTCCTTTGTTAACTGCCCATTTGAAATTTGCTCTCATCTGATCCT 1119
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 GGCCTGGGATTTCCGTACCCCGGAAATGCCAAATTTGTCAATGTCTGCAACTGGATCCT 481

QY 1120 GTCCTTTATCTGCGCATTTCTCTGAAGCGAT 1149
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 CTCCTTCCTCAATTTGCTGCTGCCCGTAATGTT 511

Search completed: December 12, 2002, 14:31:28
Job time : 211 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 09:59:17 ; Search time 141 Seconds
(without alignments)
8928.426 Million cell updates/sec

Title: US-09-931-157-1
Perfect score: 4105
Sequence: 1 gaattcgccgcctcttg.....taaaagttacagaacacctt 4105.

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	406.2	9.9	1321	4	US-09-175-658B-20
3	395.8	9.6	1873	4	US-08-910-864-13
4	395.8	9.6	4301	4	US-08-121-446-3
5	101.8	2.5	1700	5	PCT-US92-02091-1
6	91	2.2	1726	5	PCT-US92-02091-3
7	79.6	1.9	1205	3	US-09-120-772-1
8	68.6	1.7	1352	5	PCT-US92-02091-7
9	65.8	1.6	1584	5	PCT-US92-02091-5
10	63.6	1.5	1563	1	US-08-279-590A-1
11	63.6	1.5	1563	1	US-08-910-092-1
12	51.4	1.3	3095	6	5231168-1
13	46.8	1.1	1981	4	US-08-387-707-15
14	46.8	1.1	1981	4	US-08-405-271A-15
15	46.2	1.1	595	1	US-08-784-289-1
16	46	1.1	2563	2	US-08-553-436A-7
17	45.8	1.1	19124	2	US-08-487-826B-13
18	44.8	1.1	1443	3	US-08-959-381A-3
19	44.8	1.1	1626	3	US-08-959-381A-4
20	44.2	1.1	1610	3	US-08-889-108-7
21	44.2	1.1	1610	5	PCT-US94-10358-7
22	44.2	1.1	2160	4	US-08-188-275A-1
23	44.2	1.1	2162	4	US-09-351-198-1
24	44.2	1.1	2162	4	US-09-113-426-1
25	44.2	1.1	4156	1	US-08-465-687A-1
26	44.2	1.1	4156	3	US-09-030-970-1
27	44.2	1.1	4156	5	PCT-US94-11843-1

28	43.6	1.1	1422	1	US-08-319-704-5
29	43.6	1.1	8700	2	US-08-392-625-16
30	43.6	1.1	8700	2	US-08-466-961A-16
31	43.6	1.1	8700	2	US-08-645-193B-18
32	43.4	1.1	1850	3	US-08-617-860B-32
33	43.4	1.1	2570	2	US-09-056-075-2
34	43.4	1.1	4098	2	US-08-605-106-4
35	43.4	1.1	7218	1	US-08-232-463-14
36	43.2	1.1	1080	2	US-08-103-170-3
37	43.2	1.1	1419	2	US-08-103-170-5
38	43	1.0	1080	3	US-08-602-809-3
39	43	1.0	1080	5	PCT-US95-16472-3
40	42.4	1.0	6124	4	US-08-213-419B-3
41	42	1.0	665	2	US-08-883-798A-36
42	42	1.0	20674	4	US-09-641-638-651
43	41.8	1.0	5852	1	US-07-867-106-2
44	41.6	1.0	20674	4	US-09-641-638-651
45	41.2	1.0	2463	1	US-08-370-542-1

ALIGNMENTS

RESULT 1
US-08-121-446-1
; Sequence 1, Application US/08121446
; Patent No. 6313276
; GENERAL INFORMATION:
; APPLICANT: IMURA, HIROO
; APPLICANT: NAKAO, KAZUWA
; APPLICANT: NAKANISHI, SHIGETADA
; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 485..1768
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 545
US-08-121-446-1

Sequence 5, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 32, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 14, Appl
Sequence 3, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 36, Appl
Sequence 651, App
Sequence 2, Appli
Sequence 651, App
Sequence 1, Appli

Query Match				100.0%; Score 4105; DB 4; Length 4105;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 4105; Conservative				0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GAATTCGGCGCCGCTTTCGGGTCCCGAGAGTGGAGTGGAGGCTCGAGGCTTGGGAGG	60				
DB	1	GAATTCGGCGCCGCTTTCGGGTCCCGAGAGTGGAGTGGAGGCTCGAGGCTTGGGAGG	60				
QY	61	AGACGGGGAGGACAGACTGGAGGCGTCTTCCTCGGAGTTCCTTTTCCTGGGAGCCCT	120				
DB	61	AGACGGGGAGGACAGACTGGAGGCGTCTTCCTCGGAGTTCCTTTTCCTGGGAGCCCT	120				
QY	121	CGCGCGGCGTACAGTCATCCCGTGGTCTGACGATTTGTGGAGGCGGTGGAGGCTT	180				
DB	121	CGCGCGGCGTACAGTCATCCCGTGGTCTGACGATTTGTGGAGGCGGTGGAGGCTT	180				
QY	181	CATCCATCCACCCGCTGCGCGGGGATGGGGTCCCGAGACACCTCCCGGGAGAA	240				
DB	181	CATCCATCCACCCGCTGCGCGGGGATGGGGTCCCGAGACACCTCCCGGGAGAA	240				
QY	241	GCAATGCCAGGAAATTTCTGAAGCCGGGAAAGCTGTGACGCGGAGCCGCGCGCGC	300				
DB	241	GCAATGCCAGGAAATTTCTGAAGCCGGGAAAGCTGTGACGCGGAGCCGCGCGCGC	300				
QY	301	CGGAGCCCGGGACACCGGCCACCCCTCGCGCCACCCACCCCTTCCTTCCTCCCTC	360				
DB	301	CGGAGCCCGGGACACCGGCCACCCCTCGCGCCACCCACCCCTTCCTTCCTCCCTC	360				
QY	361	TGGCCCGAGGCGCGCGGACCGGAGCTGTGCGCAGCCGCGAGCTCCACGCTGAGAA	420				
DB	361	TGGCCCGAGGCGCGCGGACCGGAGCTGTGCGCAGCCGCGAGCTCCACGCTGAGAA	420				
QY	421	AAAAAGTGAAGTGTAAAGCACACAGTGCATTAAGAGATATTTCCCTCAATTTGCCT	480				
DB	421	AAAAAGTGAAGTGTAAAGCACACAGTGCATTAAGAGATATTTCCCTCAATTTGCCT	480				
QY	481	CAAGATGGAACCCCTTTTGCTCAGGCGATCCTTTTGCTGCGACTGGTGGATGTGTAAT	540				
DB	481	CAAGATGGAACCCCTTTTGCTCAGGCGATCCTTTTGCTGCGACTGGTGGATGTGTAAT	540				
QY	541	CAGTGATATCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACAC	600				
DB	541	CAGTGATATCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTCACAC	600				
QY	601	TTTTCGTGGCAGAGCTCAGCTTCCTGGTACCACATCAACCCACATATTTGGTCCCT	660				
DB	601	TTTTCGTGGCAGAGCTCAGCTTCCTGGTACCACATCAACCCACATATTTGGTCCCT	660				
QY	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACACAGAGCTAAATTAATTCAGCTTT	720				
DB	661	ACCCAGCAATGGCTCAATGCACAACTATTGCCACACAGAGCTAAATTAATTCAGCTTT	720				
QY	721	CAATATACATTAACACTGTGATATCTTTGTAATTTTCATCGTGGGAATGGTGGGAATGC	780				
DB	721	CAATATACATTAACACTGTGATATCTTTGTAATTTTCATCGTGGGAATGGTGGGAATGC	780				
QY	781	AACTCTGCTCAGGATCATTTACAGAACAAATGTATGAGGAATGGCCCAACCGCTGAT	840				
DB	781	AACTCTGCTCAGGATCATTTACAGAACAAATGTATGAGGAATGGCCCAACCGCTGAT	840				
QY	841	AGCCAGCTTGGCTTGGAGAGCTTATCTATGTGGTCAATTCCTCCCTATCAATCATTT	900				
DB	841	AGCCAGCTTGGCTTGGAGAGCTTATCTATGTGGTCAATTCCTCCCTATCAATCATTT	900				
QY	901	TAAGTGTGCTGGCGCTGGCCCTTTTGATCACAAATGACTTTGGCGTATTTCTTTGCAA	960				
DB	901	TAAGTGTGCTGGCGCTGGCCCTTTTGATCACAAATGACTTTGGCGTATTTCTTTGCAA	960				
QY	961	GCTGTTCCTCTTTTGCAGAACTCTCGGTGGGATCACCGTCCCTCAACCTCTCGCCTCT	1020				
DB	961	GCTGTTCCTCTTTTGCAGAACTCTCGGTGGGATCACCGTCCCTCAACCTCTCGCCTCT	1020				

QY	1021	TAGTGTTCACAGGTACAGAGCAGTTGGCTCCTGGAGTCTGTTCAGGGAATTTGGATTC	1080
DB	1021	TAGTGTTCACAGGTACAGAGCAGTTGGCTCCTGGAGTCTGTTCAGGGAATTTGGATTC	1080
QY	1081	TTTGGTAACTGCCATGAAATGTCTCCATCTGGATCCTCTTATCTCTGGCAATTC	1140
DB	1081	TTTGGTAACTGCCATGAAATGTCTCCATCTGGATCCTCTTATCTCTGGCAATTC	1140
QY	1141	TGAAGCCATTTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
DB	1141	TGAAGCCATTTGGCTTCGTCATGGTACCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
QY	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGCT	1260
DB	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGCT	1260
QY	1261	CTTGGGTTCTATTTCTGTATGCCCCTTGGTGTGCAGTTCCTTCTACACCCCTCATGAC	1320
DB	1261	CTTGGGTTCTATTTCTGTATGCCCCTTGGTGTGCAGTTCCTTCTACACCCCTCATGAC	1320
QY	1321	TTGTGAGATCTTGAACAGAGGAATGGCAGCTTTCAGAAATTCGCCCTCAGTGAACATCTTAA	1380
DB	1321	TTGTGAGATCTTGAACAGAGGAATGGCAGCTTTCAGAAATTCGCCCTCAGTGAACATCTTAA	1380
QY	1381	GCAGCGTCGAGAGTGGCAAAACAGTTTCTGCTTGGTGTGTAATTTTGTCTTTGCTG	1440
DB	1381	GCAGCGTCGAGAGTGGCAAAACAGTTTCTGCTTGGTGTGTAATTTTGTCTTTGCTG	1440
QY	1441	GTTCCCTCTTCACTTAAAGCCGTATATTGAAGAAACCTGTGTATACGAAATTTGGAAGAA	1500
DB	1441	GTTCCCTCTTCACTTAAAGCCGTATATTGAAGAAACCTGTGTATACGAAATTTGGAAGAA	1500
QY	1501	CGATGTGAATTTACTTACTTCTTCTGCTCATCGATTCATCGGTATTAATCTTGGCAAC	1560
DB	1501	CGATGTGAATTTACTTACTTCTTCTGCTCATCGATTCATCGGTATTAATCTTGGCAAC	1560
QY	1561	CATGAATTCATGTATAAACCCCATAGCTCTGATTTTGTGAGCAAGAAATTTAAATTTG	1620
DB	1561	CATGAATTCATGTATAAACCCCATAGCTCTGATTTTGTGAGCAAGAAATTTAAATTTG	1620
QY	1621	TTTCCAGTCAATGCTCTGCTGCTGCTTACCAGTCCAAAGTCTGATGACCTCGGTCCC	1680
DB	1621	TTTCCAGTCAATGCTCTGCTGCTGCTTACCAGTCCAAAGTCTGATGACCTCGGTCCC	1680
QY	1681	CATGAAGGGAACAAAGCATCCAGTGGGAAGAACCCAGATCAAAACACCAACAGACCG	1740
DB	1681	CATGAAGGGAACAAAGCATCCAGTGGGAAGAACCCAGATCAAAACACCAACAGACCG	1740
QY	1741	GAGCAGCATTAAGGACAGATGAACCTGACCAACCTTGAAGCACTCTCTCTCTGATC	1800
DB	1741	GAGCAGCATTAAGGACAGATGAACCTGACCAACCTTGAAGCACTCTCTCTCTGATC	1800
QY	1801	AATCTCTCGGAGAAATAATCAAGCAACTGTGACTCCGGGAATCTCTCTCTGATC	1860
DB	1801	AATCTCTCGGAGAAATAATCAAGCAACTGTGACTCCGGGAATCTCTCTCTGATC	1860
QY	1861	CTTCTCTCTTAATTTCACTCCACACCCCAAGAAATGCTTTTCCAAACCCCAAGGTAGA	1920
DB	1861	CTTCTCTCTTAATTTCACTCCACACCCCAAGAAATGCTTTTCCAAACCCCAAGGTAGA	1920
QY	1921	CTGCTTTATCCACCAACATCTACGAATCGTACTTCTTAAATTTGATCTAATTTACATA	1980
DB	1921	CTGCTTTATCCACCAACATCTACGAATCGTACTTCTTAAATTTGATCTAATTTACATA	1980
QY	1981	TTCTGGCTGTGTATTCAGCACTTAAATAATGGTGGAGCTGGGGGAGAAATCAAGACTGTT	2040
DB	1981	TTCTGGCTGTGTATTCAGCACTTAAATAATGGTGGAGCTGGGGGAGAAATCAAGACTGTT	2040
QY	2041	AAATGAACCAAGGATATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGG	2100
DB	2041	AAATGAACCAAGGATATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGG	2100
QY	2101	CTAGCTTTTATGCGAGTTCGTGGTGAATGTCAATGGGAACCTGGTCACCATTAACCTTTAG	2160

[illegible]

RESULT. 2

RES001 12
US-09-175-658B-20
Sequence 20, Application US/09175658B
Patent No. 6372900
GENERAL INFORMATION:
APPLICANT: METALLINOS, DANIKA
APPLICANT: RINE, JASPER
APPLICANT: BOWLING, ANN
TITLE OF INVENTION: HORSE ENDOTHELIUM
FILE REFERENCE: G08B-110

; CURRENT APPLICATION NUMBER: US/09/175,658B
 ; CURRENT FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: 60/062,562
 ; PRIOR FILING DATE: 1997-10-21
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 1321
 ; TYPE: DNA
 ; ORGANISM: Horse
 US-09-175-658B-20

Query Match 9.9%; Score 406.2; DB 4; Length 1321;
 Best Local Similarity 67.2%; Pred. No. 1.6e-95;
 Matches 630; Conservative 0; Mismatches 283; Indels 24; Gaps 3;

QY 717 CTTTCAATACATTAACACGTGTATCTGTATCTATTTTTCATCGTGGGAATGGTGGGA 776
 Db 310 CTTTCAAGTACATCAACACAGTAGTCTGCTGCTAGTGTCTGCTGGGATCATCGGAA 369
 QY 777 ATGCAACTGCTCAGGATCATTTACAGAACAAATGTATGAGGAATGGCCCAACGCGC 836
 Db 370 ACTCCACACTGCTGAGAATCAATTACAAGAACAAAGTGCATGCGGACGCGCTAATATCT 429
 QY 837 TGNATCCAGTCTTGCCCTGGAGACCTTATCTATGTGGTCAATGATCTCCCTATCAATG 896
 Db 430 TGATCCGACGCTGCTCCGAGACCTGCTGCAAAATCATATTGACGTCGCCATCAATG 489
 QY 897 TATTAAAGCTGCTGCTGGGCGTGGCCCTTTTTCATCACAATGACTTTGGGTATTTCTTT 956
 Db 490 TCTAAGCTGCTGGCTGAGGACTGGCC-----CTTGGAGTGCAGATGT 534
 QY 957 GCAAGCTGTTCCCTTTTTCGAGAAGTCTCGTGGGGATCACCGCTCAACCTCTGCG 1016
 Db 535 GTAAGCTGCTGCTTTCATACAGAGCGCTCCGCTGGGATCATCTGCTGAGTCTGTG 594
 QY 1017 CTCCTAGCTGACAGGTACAGAGAGTGGCCCTCGGAGTCTGTTACAGGGAATGGGA 1076
 Db 595 CTCCTAGTATGACAGATACGAGTGTGCTTCTTCTTGGAGCAATTAAGGAATTCGGG 654
 QY 1077 TTCCTTTGTAAGTGCATTAATGTTCTCCATCTGGATCTGCTTATCTCTGCGCA 1136
 Db 655 TTCCAAATGAGACAGAGTAAATGTTTAAATTTGGGTGGTCTCTGTTGTTCTGCTG 714
 QY 1137 TTCCTGAAGCAGTATGCTTCTGCTGATGCTACCTTTTCAATATGAGGTGAACAGCATAA 1196
 Db 715 TCCCTGAAGCAGTATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 774
 QY 1197 CTTGATGCTCAATGCCAC-----ATCAAAATTCAGGAGTCTTACCAAGATGTAAAG 1250
 Db 775 TCTGCTGCTTCTATCCCACTCAGAAACAGCCTTTCATGAGTCTTACAGAAATGCTAAG 834
 QY 1251 ACTGTGCTCTTCGGTCTATTTCTGTATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 1310
 Db 835 ACTGTGCTCTATTTAGTTCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
 QY 1311 CCTCATGACTTGTGAGATGTTGAACAGAAAGTGGAGCTTGAGAAATGCTGCTGCTGCTGCT 1370
 Db 895 CTTGATGACTGTGAATGTTGAGAAAGAGAGTGCA---TGCAAAATGCTTAAAG 951
 QY 1371 AACATCTTAAAGCAGGCTGAGAGTGGCAAAACAGTCTTCTGCTGCTGCTGCTGCTGCTGCT 1430
 Db 952 ATCACTTAAAGCAGAGAGAGAGTGGCAAAACAGTATTTCTGCTGCTGCTGCTGCTGCTGCT 1011
 QY 1431 CTCCTTGTGCTTCT 1490
 Db 1012 CCTGTGCTGCTTCT 1550
 QY 1491 TGGCAAGAACCGATGCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1550
 Db 1072 ATGATCCCCATAGATGAACCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131
 QY 1551 ACTTGGCAACCATGAATTCATGATATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAAT 1610

Db 1132 ACATGGCTCCCTCCGAATTCCTGCAATTAATCAATAGTCTCTATTTGCTGAGCAAGAT 1191
 QY 1611 TTAATAATTTGTTTCCAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1647
 Db 1192 TCATAAACTGCTTAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1228

RESULT 3
 US-08-910-864-13
 ; Sequence 13, Application US/08910864
 ; Patent No. 6280931
 ; GENERAL INFORMATION:
 ; APPLICANT: SAKAMOTO, AIJI
 ; APPLICANT: HANAOKA, FUMIO
 ; TITLE OF INVENTION: METHOD FOR SPECIFICALLY AMPLIFYING A CDNA OF AN EXTREMELY
 ; TITLE OF INVENTION: SMALL QUANTITY
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FISH & RICHARDSON P.C.
 ; STREET: 4225 EXECUTIVE SQUARE, SUITE 1400
 ; CITY: LA JOLLA
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,864
 ; FILING DATE: 13-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 216506/1996
 ; FILING DATE: 16-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HAILE, LISA A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07998/017001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-678-5070
 ; TELEFAX: 619-678-5099
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1873 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA to mRNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 231..1556
 ; US-08-910-864-13

Query Match 9.6%; Score 395.8; DB 4; Length 1873;
 Best Local Similarity 65.7%; Pred. No. 9.3e-93;
 Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

QY 689 TGCCACAGCAGACTAAATTTACTTTCAGCTTCAAAATACATTAACATCTGTGATCTTGT 748
 Db 498 TGCCAGGAGCCATCCAGATCAAGGAGACTTCAATACATCAACAGGTTGTCTCTGC 557
 QY 749 ACATTTTTCATCTGGGAATGGTGGGAATGCAACCTCTGCTCAGGATCATTTACCAGAAC 808
 Db 558 CTTGTGCTGCTGCTGGGATCATCGGGAACCTCCACACTTCTGAGAAATATCTACAAGAAC 617
 QY 809 AATGATGATGAGGAATGGCCCAACGCTGATAGCCAGTCTTGGCCCTTGGAGACCTTATC 868
 Db 618 AAGTGCATCGAAGCGTCCCAATATCTTTGATGCCAGCTTGGCTTGGGAGACCTGCTG 677
 QY 869 TATGTGCTCATTCATCTCCCTATCAATGATTTTAAAGCTGCTGCTGCTGCTGCTGCTT 928

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Db 678 CACATCGTCATGATCCCTATCAATGCTCTACAGCTGCTGGCAGAGACTGGCC----- 733
QY 929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTCTTTTCCAGAAGTCCCTCG 988
Db 734 -----ATTGGAGCTGAGATGTTAGCTGGTCTTTCATACAGAAAGCTCC 782
QY 989 GTGGGGATCACCCTCAACCTCTGGCTCTTAGTGTGACAGGTACAGAGAGTTCGCC 1048
Db 783 GTGGGAATCACTGTGCTGAGTCTATGCTCTGAGTATTGACAGATATGAGCTGTTGCT 842
QY 1049 TCTGGAGTGTGTTCAAGGAATTTGGATTCCTTTGTTAACTGCAATGCAATGCAATGCTCC 1108
Db 843 TCTTGGAGTAGAATTAAGGAATTTGGGTTTCCAAAATGGACAGCAGTAGAATAATGTTTG 902
QY 1109 ATCTGGATCTGCTCTTTATCTCTGGCATTCCTCAAGCGATTGCTGCTGATGTCACCC 1168
Db 903 ATTTGGGTGCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 962
QY 1169 TTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
Db 963 ATGGACTACAAAGGAAGTTATCTCGAATCTGCTTCTTCATCCGTTTCAGAACAGAGCT 1022
QY 1223 TTTATGAGCTTCTACCAAGATGTTAAAGAGCTGTTGGCTCTTTCCGGTCTATTTCTGTATG 1282
Db 1023 TTTATGAGCTTCTACCAAGATGTTAAAGAGCTGTTGGCTCTTTCCGGTCTATTTCTGTATG 1082
QY 1283 CCCTTGGTGTGCACTGCTGATCTTCTACACCTCATGACTGTGAGATGTTGAACAGAGG 1342
Db 1083 CCATTTGGCCATCACTGCTGATTTTATATACACTAATGACCTGTGAATGTTG---AGAAAG 1139
QY 1343 AATGGAGCTTGTGAGAAATTTGGCTCAGTGAACATCTTAAGCAGCTCGAGAGGTGGCAAAA 1402
Db 1140 AAAAGTGGCATGAGATGCTTTAAATGATCACCCTAAAGCAGAGACGGGAGTGGCCAAA 1199
QY 1403 ACAGTCTTCTGCTGCTGTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1462
Db 1200 ACCGCTCTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1259
QY 1463 ATATTGAAGAAACTGTGTATACGAATATGGAAGTGAACAGACGATGTAATGTAATGTTTC 1522
Db 1260 ATTTCAAGCTCACTCTTTAATATCAAGAAATGATCCCAATAGATGTAATGTAATGTTTC 1319
QY 1523 TTAAGCTCTGATGATACATCGGTATTAATGTTGCAACCACTGATGATGATGATGATGATG 1582
Db 1320 CTGTTGGTATGCACTATATGTTATCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1379
QY 1583 ATAGCTCTGATTTTGTGAGCAAGAAATTTTAAATTTGTTTCCAGTCACTGCTGCTGCTG 1642
Db 1380 ATGCTCTGATTTTGTGAGCAAGAAATTTTAAATTTGTTTCCAGTCACTGCTGCTGCTG 1439
QY 1643 TGCTG 1647
Db 1440 TGCTG 1444
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RESULT 4
US-08-121-446-3
; Sequence 3, Application US/08121446
; Patent No. 6313276
; GENERAL INFORMATION:
; APPLICANT: IMURA, HIROO
; APPLICANT: NAKAO, KAZUHA
; APPLICANT: NAKANISHI, SHIGETADA
; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,446
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/911,684
FILING DATE: 10-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 29900-20324.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 238..1566
US-08-121-446-3

Query Match 9.68; Score 395.8; DB 4; Length 4301;
Best Local Similarity 65.7%; Pred. No. 1.4e-92;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;
QY 689 TGCCACAGCAGACTAAATTTACTTTCAGCTTTTCAATATACATTAAACACTGTGATATCTCT 748
Db 505 TGCCAGGACCCATCGAGATCAAGAGACTTTCATATACATCAACACGGTGTGCTCTGC 564
QY 749 ACTATTTTCATCGTGGGAATGTTGGGAATGCACTCTGCTCAGGATCATTTTACCAGAAC 808
Db 565 CTTCGTGCTGCTGGGATCATCGGAACTCCACACTTCTGAGAATTTATCTACAAGAAC 624
QY 809 AAATGATAGAGATGCCCCCAACGCGTGATAGCCAGCTTGGCCCTTGGAGACCTTATC 868
Db 625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
QY 869 TATGTGTCATGATCTCCCTATCAATGATTTTAAAGCTGCTGGCTGGCGCTGGCTTTT 928
Db 685 CACATGCTGATGATCCCTATCAATGCTACAGCTGCTGGCAGAGACTGGCC----- 740
QY 929 GATCACAATGACTTTGGCGTATTTCTTTTSCAAGCTGTTTCCCTTTTTCAGAAAGTCTCG 988
Db 741 -----ATTTGGAGCTGAGATGTTAAAGCTGCTGCTTTCATACAGAAAGCTCTC 789
QY 989 GTGGGATCACCCTCAACCTCTGCGCTCTTAGTGTGACAGGTACAGAGACTGTGCC 1048
Db 790 GTGGGAATCACTGTGCTGAGTCTATGCTCTGAGTATTGACAGATATCGAGCTGTGCT 849
QY 1049 TCCGTGGAGTGTGTTCAAGGAATTTGGGATTTCTTTGGTAACTGCCATTGAATTTCTCC 1108
Db 850 TCTTGGAGTAGAATTAAGGAATTTGGGTTTCCAAAATGGACAGCAGTAGAATAATGTTTG 909
QY 1109 ATCTGGATCTGCTCTTTATCTCTGGCATTCCTCAAGCGATTGCTGCTGATGTCACCC 1168
Db 910 ATTTGGGTGCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969
QY 1169 TTTGAATATAGGGGTGAACAGCATAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222
Db 970 ATGGACTACAAAGGAAGTATCTCGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1029
QY 1223 TTTATGAGCTTCTACCAAGATGTTAAAGAGCTGTTGGCTCTTCCGGTCTTATTTCTGTATG 1282
Db 1223 TTTATGAGCTTCTACCAAGATGTTAAAGAGCTGTTGGCTCTTCCGGTCTTATTTCTGTATG 1282

Query Match 2.5%; Score 101.8; DB 5; Length 1700;
Best Local Similarity 49.3%; Pred. NO. 1.4e-16;
Matches 308; Conservative 0; Mismatches 302; Indels 15; Gaps

[illegible]

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RESULT 6
PCT-US92-02091-3
; Sequence 3, Application PC/TUS9202091
; GENERAL INFORMATION:
; APPLICANT: Battey Jr., James F.
; APPLICANT: Corjay, Martha H.
; APPLICANT: Feldman, Richard I.
; APPLICANT: Harkins, Richard N.
; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

```

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwin P. Ching
STREET: 1501 Harbor Bay Parkway
CITY: Alameda
STATE: CA
COUNTRY: USA
ZIP: 94501
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02091
FILING DATE: 19920313
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/426,150
FILING DATE: 24-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/533,659
FILING DATE: 05-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34090
REFERENCE/DOCKET NUMBER: A-0092C
TELEPHONE: 415-266-7476
TELEFAX: 415-266-7400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1726 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Small cell lung carcinoma
CELL LINE: NCI-H345
IMMEDIATE SOURCE:
LIBRARY: Lambda Gt10
FEATURE:
NAME/KEY: CDS
LOCATION: 399..1553
CT-US92-02091-3

Query Match 2.2%; Score 91; DB 5; Length 1726;
Best Local Similarity 48.3%; Pred. No. 9.1e-14;
Matches 299; Conservative 0; Mismatches 305; Indels 15; Gaps 1;
QY 720 TCAATACATTAACACTGTGATCTGTACTATTTTCATCGTGGGAATGGTGGGAATG 779
Db 514 TTCTCTATGTCATCCCTGCGAGTTTATGGGTATCATCTGTAGAGGCTCATTTGGCAACA 573
QY 780 CAACCTGCTCAGGATCATTTACAGAACAAATGTATAGGAATGGCCCAACGCGCTGA 839
Db 574 TCACCTTGATCAAGATCTTCTGTACAGTCAAGTCCATCGCAACAGTTTCCAAACCTGTTC 633
QY 840 TAGCCAGTCTTGGCCCTGGAGACCTTATCTATGTGTGTCATGATCCCTATCAATGTAT 899
Db 634 TTTCCAGTCTGGCTTTGGGAGACCTGCTCTCTTAAGCTGTGTCTCCAGTGGATGCCA 693
QY 900 TTAAGCTGTGGCTGGCGCTGGCTTTTATCATCAATGACTTTTGGCGTATTTCTTTGCA 959
Db 694 GCAGGTACTGCTGCATGATGCTATTTGGCAGGATTGGC-----TGCA 738
QY 960 AGCTGTTCCCTTTTTCGCAAGTCTCGGTGGGGATCACCTCCCAACCTCTCGGCTC 1019
Db 739 AACTGATCCCTTTATACAGCTTACCTCTGTTGGGGTGTCTGTCTTCACACTCAGCGGC 798

QY 1020 TTAGTGTTCACAGGTACAGAGCAGTTGCTCCTGGAGTCTGTTCAGGAATTTGGGATTC 1079
Db 799 TCTCGCAGACAGATACAAAGCCATGTCCGCCAATGGATATCCAGGCTTCCCATGCC 858
QY 1080 CTTTGTAACTGCCATTTGAAATTTGTTCCATCTCGATCTGGATCTGTCTTTATCTCTGCCATTC 1139
Db 859 TGATGAAGATCTGCTCAAAAGCGCTTTATCTGGATCATCTCCATGCTGCTGCCATTC 918
QY 1140 CTGAAGCGATTTGGCTTCGTCATGGTACCTTTTGAATATAGGGGTGAACAGCATAAAACCT 1199
Db 919 CAGAGCGCGTGTCTTCTGACCTCCATCCCTTCCATGAGGAAAGCACCACAGACCTTCA 978
QY 1200 GTATGCTCAATGCCACATCAAAATTCATGAGTTCCTACCAAGATGTAAAGGACTGTGGC 1259
Db 979 TTAGCTGTGCCCATACCACACTCTAATGAGCTTCACCCCAAAATCCATTTCTATGGCTT 1038
QY 1260 TCTTCGGGTTCATTCTGTATGCCCTTGGTGTGGCTGCGACTGCGATCTTCTACACCTCATGA 1319
Db 1039 CTTTCTGCTCTTCTACGTATCCACCTCCACCTGTCGATCATCTCTGTTACTACTACTTCTATG 1098
QY 1320 CTTGTGAGATGTTGAACAG 1338
Db 1099 CTAATAATCTGATCCAGAG 1117

RESULT 7

US-09-120-772-1
; Sequence 1, Application US/09120772
; Patent No. 6143521
; GENERAL INFORMATION:
; APPLICANT: LANE, PAMELA
; APPLICANT: TSUL, PING
; APPLICANT: ELSHOUBAGY, NABIL
; TITLE OF INVENTION: HUMAN BOMBESIN RECEPTOR SUBTYPE
; TITLE OF INVENTION: 3
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,772
; FILING DATE: 22-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1205 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-120-772-1

Query Match

1.9%; Score 79.6; DB 3; Length 1205;

Best Local Similarity 46.9%; Pred. No. 6.8e-11;	
Matches 419; Conservative 0; Mismatches 439; Indels 36; Gaps 4;	
Qy	761 GTGGGAATGGTGGGGAATGCCAACTCTGCTCAGGATCATTTACCAGACAATAATGTATGAGG 820
Db	180 GTGGGACCTCTGGAAATGGCTATTCTCATCAAGTCTTTTTCAAGACCAAAATCCATGCAA 239
Qy	821 AATGGCCCAACGCGCTGATACCCAGTCTTGCCCTGGAGACCTTATCTATGTGTGCTATT 880
Db	240 ACAGTTCCAATATTTTCATCACAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACT 299
Qy	881 GATCTCCCTATCAATGTATTTAAGCTGTGGCTGGCGCTGCCCTTTTTCATCACAATGAC 940
Db	300 TGTGTGCCAGTGGATGCAACTCCTACCTTGCAGAAGGATGCGTCTTC----- 347
Qy	941 TTTGGGTATTTCTTTGCAAGCTGTTCCTTTTTCGAGAGTCTCCGGTGGGATCACCC 1000
Db	348 ---GGAAGAAATTTGGTTGAAGGTGCTCTTTTCATCCGGCTCACATCTCTGTGGTGTGCA 404
Qy	1001 GTCTTCACCTCTGCGCTTAGTCTTGACAGGTACAGAGCAGTTGCGCTCCTGGAGTCTGT 1060
Qy	405 GTGTTACATTAGCAATTTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAG 464
Qy	1061 GTTCAGGAATTTGGGATTTCCTTTGTTAACTGTCATTTGAATTTGCTCTCCATCTGGATCTGT 1120
Db	465 CGACAGCCCTCGAATGCCATCTGGAAGACTGTGTAAAGCTGGCTGGGTATGCTG 524
Qy	1121 TCCTTTATCTCGGCCATTTCCCTGAAGCGATTTGGCTTCGTATGGTACCTTTGAATATAGG 1180
Db	525 TCTATGATATTGCTCTACCTGAGGCTATATTTTCAATGTATACACTTTTCGAGATCCC 584
Qy	1181 GGTGAACAGCATAAACCTGTATGCTCAATGCCACATCAAAATTCATGGAGTTTTCACAA 1240
Db	585 AATAAAAAATAGACATTTTGAATCATGTACCTCTTATCTGCTCTTAAGAAAGCTCTTGCAA 644
Qy	1241 GATGTAAAGGACTGTGGCTCTTCGGGTTCTATTTCTGTATGCCCTTTGGTGTGCACTGGC 1300
-Db	645 GAAATACATCTCTGCTGTGCTTTAGTGTCTACATTTATCCACTCTCTATTATCTCT 704
Qy	1301 ATCTTCTACACCCTCATGACTGTGAGATGTTGAACAGAAAGGATGGCAGCTTGAGAATT 1360
Db	705 GTCTACTATTCTTGATTTGCTTAGGACCCCTTTACAAAGCACCCCTGAACATACCTACTGAG 764
Qy	1361 GCCCTCAGAACATCTTAAGCA-----CGTCGAGAAGTGGCAAAACAGTTTTTC 1411
Db	765 GAACAAAGCCATGCCCGTAAGCAGATTGAATCCCGAAAGAGAAATGGCCAGAACGGTATFG 824
Qy	1412 TGTCTGGTGTAAATTTTTCCTTTTTCGCTTTCCTCTTTCAGTTAAGCCGTATATTGAAG 1471
-Db	825 GTGTTGGTGGCTCTGTGTTGGCCCTCTGCTGGTTGGCAATCACCT--CCTGTACCTCTACC 882
Qy	1472 AAAACTGTGTATACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTCTTACTGCTC 1531
Db	883 ATTCAATTCATCTCAAAACCTATGTAGACCCTCTGCCATGCAATTTCAATTTTCACCAFT- 941
Qy	1532 ATGGATTACATCGGTATTAACTTTGGCAACCATGAATTCATGTATAAACCCCATAGCTCTG 1591
Db	942 -----TTCTCTCGGGTTTGGCTTTCAGCAATCTTCGGTAAACCCCTTTGCTCTC 992
Qy	1592 TATTTTGTGACAGAAATTTAAAAATTTTTCAGTCATGCCCTGTGCTGTGC 1645
Db	993 TACTGGGTGACAAAAGCTTCAGAAAGCATTTTAAAGCTCAGTTGCTGTCTGTGC 1046

RESULT 8

```

PC/US92-02091-7
: Sequence 7, Application PC/TUS9202091
: GENERAL INFORMATION:
: APPLICANT: Battley Jr., James F.
: APPLICANT: Corjay, Martha H.
: APPLICANT: Feldman, Richard I.
: APPLICANT: Harkins, Richard N.
: TYPE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES
:
461 GAGTGGATGTTTTGGCAAGGTGGGCTGCAAACTGATCCCTGATCCAGCTCACTTCGGT 520
Db
992 GGGATCACCGTCTCAACCTCTCGGCTCTAGTGTGACAGGTACAGAGCAGTGGCTCC 1051
QY
521 GGGGTTTCGGTGTTCACCTCTCACTGCCCTCAGCGCGACAGGTACAGAGCATCGTTAAC 580
Db
1052 TGGAGTCTGTGTTTCAGGGAATTGGGATTCCTTTTGGTAACGCCATTGAAAATTGCTCCATC 1111
QY

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Best Local Similarity 45.5%; Pred. No. 1.le-06;
Matches 332; Conservative 0; Mismatches 374; Indels 24; Gaps 2;

QY 735 CTGTGATATCTTGTACTATTTTCATCTGGGAATGGTGGGAATGCAACTCTGCTCAGGA 794
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 340 CTGTACATATGCTGTATTATTTCTGCGGTATCTTGGAAACAATACTTATAAG 399

QY 795 TCATTACAGACAAATATGACGAATGGCCCAAGCGGTGATAGCAGCTTGGCCC 854
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 400 TATTTTAAAAATCAAGTCAATGAGCTGTTCTTAATATTTTCATCACCAGCTGGCTT 459

QY 855 TTGGAGACCTTATCTATGTTGGTCAATGATCTCCCTATCAATGATTTTAACTGCTGCTG 914
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 460 TTGGAGATCTTCTTACTGCTGACCTGCGTGCAGTGGACGATCTCGGTATATTGTGG 519

QY 915 GCGCTGGCTTTTGTATCAATGATCTTGGGCTATTTCTTCAAGCTGTTCCCTCTTTT 974
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 ACACGTGGATGTTTGGAAAGCTGGCTGT-----AGATAATTTCTCTCA 564

QY 975 TGCAGAACTCTCGGTGGGATCACGCTCCTCAACCTCTGCGCTCTTAGTGTGACAGT 1034
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 565 TACAGCTTACCTCTCTGCGGAGTGTGCTGTTTACTTTAACTGTCTCAGTACTGACAGT 624

QY 1035 ACAGAGCAGTTCCTCTGAGTCTGTTTCAGGAATGGGATTCCTTTGGTAACCTGCCA 1094
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 625 ACAGAGCAGTTCGAAACCTTGCATTCGAGACCTTCAGATGCGGTTTGAAGACATGTG 684

QY 1095 TTGAAATTTCTCCCATCTGATCTGCTCTTATCTTCTGCGCTTCTTGAAGCATTTGGCT 1154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 685 GCAAAGCTGTTTGTGTTGGATCATTTCCATCTCTCTGCTGCTCAGAAAGCTGTCTTCT 744

QY 1155 TCGTCATGTCACCTTTTGAATAGGGTGAACAGATAAAAACCTGTATGCTCAATGCCA 1214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 745 CAGATTTGTATGAATTTGGCAGCTCGGAAAAAATACCACTTTTGAAGCTGTGCTCCAT 804

QY 1215 CATCAAAATTCATGAGTCTTACCAGATGTAAAGAGCTGGTCTTTCGGGTCTATT 1274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 805 ATCCAGTCTCTGAAAGATTTCTGCAAGAGACACATTTCCCTAATATGCTTCTCGGTATTCT 864

QY 1275 TCTGTATGCCCTTGGTGTGCTGCTGCTTCTTACACCTCATGACTTGTGAGATGTTCA 1334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Query Match 1.5%; Score 63.6; DB 1; Length 1563;
Best Local Similarity 45.5%; Pred. No. 1.le-06;
Matches 332; Conservative 0; Mismatches 374; Indels 24; Gaps 2;

QY 735 CTGTGATATCTTGTACTATTTTCATCTGGGAATGGTGGGAATGCAACTCTGCTCAGGA 794
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 340 CTGTACATATGCTGTATTATTTCTGCGGTATCTTGGAAACAATACTTATAAG 399

QY 795 TCATTACAGACAAATATGACGAATGGCCCAAGCGGTGATAGCAGCTTGGCCC 854
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Db 400 TATTTTAAAAATCAAGTCAATGAGCTGTTCTTAATATTTTCATCACCAGCTGGCTT 459

QY 855 TTGGAGACCTTATCTATGTTGGTCAATGATCTCCCTATCAATGATTTTAACTGCTGCTG 914
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Db 460 TTGGAGATCTTCTTACTGCTGACCTGCGTGCAGTGGACGATCTCGGTATATTGTGG 519

QY 915 GCGCTGGCTTTTGTATCAATGATCTTGGGCTATTTCTTCAAGCTGTTCCCTCTTTT 974
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 ACACGTGGATGTTTGGAAAGCTGGCTGT-----AGATAATTTCTCTCA 564

QY 975 TGCAGAACTCTCGGTGGGATCACGCTCCTCAACCTCTGCGCTCTTAGTGTGACAGT 1034
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 565 TACAGCTTACCTCTCTGCGGAGTGTGCTGTTTACTTTAACTGTCTCAGTACTGACAGT 624

QY 1035 ACAGAGCAGTTCCTCTGAGTCTGTTTCAGGAATGGGATTCCTTTGGTAACCTGCCA 1094
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Db 625 ACAGAGCAGTTCGAAACCTTGCATTCGAGACCTTCAGATGCGGTTTGAAGACATGTG 684

QY 1095 TTGAAATTTCTCCCATCTGATCTGCTCTTATCTTCTGCGCTTCTTGAAGCATTTGGCT 1154
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Db 685 GCAAAGCTGTTTGTGTTGGATCATTTCCATCTCTCTGCTGCTCAGAAAGCTGTCTTCT 744

QY 1155 TCGTCATGTCACCTTTTGAATAGGGTGAACAGATAAAAACCTGTATGCTCAATGCCA 1214
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Db 745 CAGATTTGTATGAATTTGGCAGCTCGGAAAAAATACCACTTTTGAAGCTGTGCTCCAT 804

QY 1215 CATCAAAATTCATGAGTCTTACCAGATGTAAAGAGCTGGTCTTTCGGGTCTATT 1274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 805 ATCCAGTCTCTGAAAGATTTCTGCAAGAGACACATTTCCCTAATATGCTTCTCGGTATTCT 864

QY 1275 TCTGTATGCCCTTGGTGTGCTGCTGCTTCTTACACCTCATGACTTGTGAGATGTTCA 1334
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RESULT 11
US-08-910-092-1
; Sequence 1, Application US/08910092
; Patent No. 5814463
; GENERAL INFORMATION:
; APPLICANT: Spindel, Eliot R.
; APPLICANT: Nagalla, Srinivasa
; APPLICANT: Barry, Brenda
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RECEPTORS
; TITLE OF INVENTION: FOR HOMBESIN-LIKE PEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US

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Db 865 ACATTGTTCCCTGTCATCAATCAATTTCTGCATATTTACTTCCCTATTTGCAAAACCCCGTGA 924
Qy 1335 A-----CAGAAGGAATGGCAGCTTGAGAATTCCTCAGTGAACATCTTAAGCAGC 1385
Db 925 AAAGTACTTTCAACATGCTCTGNAGAGCACACACGCGCGGAACAGATAGATCGC 984
Qy 1386 GTCGAGAAGTGGCAAAACAGTTTCTGCTGGTGTGAATTTTGTCTCTTTGCTGGTTC 1445
Db 985 GCAACAGAGTGGCAAAACAGTTTCTGCTGGTGTGGTGGCATTTGTCGACGTGCTGGTTC 1044
Qy 1446 CTCCTCACTT 1455
Db 1045 CAACACCAT 1054

RESULT 12
5231168-1/c
Patent No. 5231168
APPLICANT: DIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SOREN;
VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H.
TITLE OF INVENTION: MALARIA ANTIGEN
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
FILING DATE: 18-SEP-1989
SEQ ID NO: 1:
LENGTH: 3095
5231168-1

Query Match 1.3%; Score 51.4; DB 6; Length 3095;
Best Local Similarity 42.6%; Pred. No. 0.0023;
Matches 335; Conservative 0; Mismatches 446; Indels 6; Gaps 1;

Qy 2151 GAACATTTAGAGATTAACGACAGATTTTCTACTTTTAAAGTGAATTTTGTCCCTTCA 2210
Db 2999 GACATTATAAACTTACTTTTCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTA 2940
Qy 2211 GCCAAACACATATGGCTCAGGTCACCTTTTATTTGAATGTCATTTGGTCCCATTTT 2270
Db 2939 TTTAAATTTAAATAATATATATGAATTTTATACCTTAAGAAATATAATCAGACATAG 2880
Qy 2271 TTTAACTGCATAATAGCTAACATGATTTTGAACATTTTACACATAGTTTGAAGAAA 2330
Db 2879 ATTATTTGTTTCATATTTTATTTGCAATTTATGCCAAAGGCAACATGATATATATAA 2820
Qy 2331 AAAGACAAAATAGTATTCAGGTCAGCAATTAGATTTAGTATTTTCCAGCTCATTTTA 2390
Db 2819 TATATACATAAATTTATCCAGTATTTATATATAATAATTTATTTATATAATTTATGAAA 2760
Qy 2391 TTTTAAACACAAATTTCTAAAGCTACACAAATTTACTACAGCCCTTAAAGCACAGTC 2450
Db 2759 AAATGATATAAATAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2700
Qy 2451 TGATGACACATTTGGCAGTTTAAATAGATTTTACTCAAGAAATTTTAAAGAACTGATTT 2510
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Qy 2511 TATTTTAAATGGTGTGTTTATTAACAGGACCTTTGAACATGTTTGTATGTTAAATTTCA 2570
Db 2639 TTTTATTTATACATGATATCTTCAATTAATAAATAATTTTCTTCTTCTTCTTCTTCTTCTT 2580
Qy 2571 AAAGTAAATGCTTCATACAGATGTTCTTTTTCACAAAGTTCATGTTTCTTCTTCTTCTT 2630
Db 2579 TTTTATTTATTTTATAGAAATTAATAACAACTAAGAAAGAAATTTATTTATTTATTTT 2520
Qy 2631 TTTTGTATGAAATCAATCAATGCAAGTACCAAAATGTTAATGATGTTGTCATTTAACTG 2690
Db 2519 TTTCTAATAATATACAAATGAATTTATTTCTATATATACAGAAATCTAGTATTTCTTTA 2460
Qy 2691 CCTGAGACTTTCACTGCTATATAGAAAGTCTTAAACACACACATAGAGAAAAGATCG 2750
Db 2459 TATAATATATATTTTATTAATAATAATATATAGTTTACTTACATATATAAGAAAAAATTT 2400

Qy 2751 A-----ATTTTCAGATGATTCGGAATTTTTCATTTCAGTATTTGTAAATGATGACATAT 2804
Db 2399 ATTTAATAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2340
Qy 2805 ATATGATATACATATACACCTCTCTATCTCTTAAATTTTGTGTTAAATGTTAACTGGCAGT 2864
Db 2339 AAAAAATATACATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2280
Qy 2865 AAGTCTTTTTCATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2924
Db 2279 TCATATGATTAATCATACACTTACATAGTTTGTAGATCTTTTAAATTTCTTTGTA 2220
Qy 2925 AGTTTAT 2931
Db 2219 GATATAT 2213

RESULT 13
US-08-387-707-15
Sequence 15, Application US/08387707
Patent No. 6265563
GENERAL INFORMATION:
APPLICANT: EVANS, CHRISTOPHER J.
APPLICANT: KEITH, DUANE E.
TITLE OF INVENTION: OPIOID RECEPTOR GENES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, N.W. Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,707
FILING DATE: 10-SEP-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20526.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-387-707-15

Query Match 1.1%; Score 46.8; DB 4; Length 1981;
Best Local Similarity 51.4%; Pred. No. 0.028;
Matches 108; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 940 CTTTGGCGTATTTCTTTCGAGCTGTTCCCTTTTTCGAGAGAGTCTCGGTGGGATCAC 999
Db 657 CTTTGGAAACATCTCTTCGAAAGATCGTATCTCAATAGACTACTACAACATGTTCCACAG 716
Qy 1000 CGTCTCAACCTCTCGGCTCTTAGTGTTCAGAGGTACAGAGCAGTTGCCCTCTCGGAGTCG 1059
Db 717 TATCTTCACCTCTGCGACCATGAGTGTAGCCGCTACATTTGCCCTGTCACCCCGTCAA 776
Qy 1060 TGTTCAGGAATTTGGGATTTCTTTTGTAACTGCCCATTTGAAATTTGTCTCCATCTGGATCCT 1119
Db 777 GGCCCTGATTTCCGTACCCCGGAAATGCCAAATTTGTCAATGTCTGCACTGATCTCT 836

QY 1120 GTCTTTATCTGCGCATTCCTGAAGCGAT 1149
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Db 837 CTCTTCTGCGCATTTGGTCTGCCCGTAATGTT 866

RESULT 14

US-08-405-271A-15
; Sequence 15, Application US/08405271A
; Patent No. 6432652
; GENERAL INFORMATION:
; APPLICANT: EVANS, CHRISTOPHER J.
; TITLE OF INVENTION: OPIOID RECEPTOR GENES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, Suite 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,271A
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20526.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-405-271A-15

Query Match 1.1%; Score 46.8; DB 4; Length 1981;
Best Local Similarity 51.4%; Pred. No. 0.028;
Matches 108; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
940 CTTTGGCGTATTCTTTGCAAGCTGTTCCCTTTTGGCAGAGTCTCGTGGGATCAC 999
||| | | | | | | | | | | | | | | | |
Db 657 CTTTGGAAACATCTCTGCAAGATCGTGATCTCAATAGACTACTACAACATGTTCCACGAG 716
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QY 1000 COTCTCAACCTCTCGGCTCTTAGTGTGACAGAGTACAGACGAGTTGCCCTCGGAGTCG 1059
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QY 1060 TGTTCAGGGAATTGGGATTCCTTTGGTAACTGCCATTGAAATGTCTCCATCTGGATCCT 1119
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Db 777 GGCCCTGGATTTCCGCTACCCCGCAAAATGTGCAATGTCTGCAACTGGATCCT 836
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QY 1120 GTCTTTATCTGCGCATTCCTGAAGCGAT 1149
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Db 837 CTCTTCTGCGCATTTGGTCTGCCCGTAATGTT 866

RESULT 15

US-08-784-289-1
; Sequence 1, Application US/08784289
; Patent No. 581912
; GENERAL INFORMATION:
; APPLICANT: Pedrazzini, Thierry

APPLICANT: Brunner, Hans R
TITLE OF INVENTION: Transgenic Animals with Disrupted NPY Y1
RECEPTOR GENES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins L.L.P.
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,289
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BMR 350/13000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-6585
TELEFAX: (202) 639-6604
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-784-289-1

Query Match 1.1%; Score 46.2; DB 1; Length 595;
Best Local Similarity 50.7%; Pred. No. 0.021;
Matches 111; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 711 CTTACGCTTTCAATACATTAAACACGTGTGATATCTTGTACTATTTTTCATCGTGGGAATGG 770
||| | | | | | | | | | | | | | | | |
Db 45 CCTTGGCTGTGATATTACCTTAGCTTGTCTTATGGGCTGTGATATTCTTGGGTCT 104
||| | | | | | | | | | | | | | | | |
QY 771 TGGGGAATGCACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCA 830
||| | | | | | | | | | | | | | | | |
Db 105 CTGGAAACCTGGCATTGATCATTAATCATCTCTAAACACAGAGAGATGAGGAATGTACCA 164
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QY 831 ACAGCGTGTATAGCCAGCTTGGCCCTTGGAGACCTTATCTATGTGGTCATGATGATCCCTA 890
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Db 165 ACATTCGTGATCGTGAACCTCTCCTTCTCAGACTTGTCTGTCGAGCATCATGTCTCCCGT 224
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QY 891 TCAATATATTAAAGCTGCTGGCTGGCGCTGGCTTTTG 929
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Search completed: December 12, 2002, 14:28:11
Job time: 169 secs

GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 08:12:06 ; Search time 761 Seconds
(without alignments)
12147.770 Million cell updates/sec

Title: US-09-931-157-1

Perfect score: 4105

Sequence: 1 gaattcgccgcctcttg.....taaaagtattacagaacacctt 4105

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4103.4	100.0	4105	14	AAQ34583
2	4103	100.0	4105	21	AAQ34583
3	2470	60.2	2595	24	AAQ34583
4	2470	60.2	2595	24	AAQ34583
5	2470	60.2	2595	24	AAQ34583
6	1819.6	44.3	1868	21	AAQ34583
7	1819.6	44.3	1868	21	AAQ34583
8	1819.6	44.3	1868	21	AAQ34583
9	1819.6	44.3	1868	21	AAQ34583

10	1819.6	44.3	2008	21	AAF20904	Human low adenosin
11	1819.6	44.3	2008	21	AAQ34782	Human adenosine re
12	1819.6	44.3	5036	21	AAQ21447	Human endothelin r
13	1819.6	44.3	117609	21	AAQ21435	Human receptor-rel
14	1296.8	31.6	1310	21	AAF20902	Human endothelin r
15	1296.8	31.6	1310	21	AAF20914	Human ELAM-1 polyn
16	1296.8	31.6	1310	21	AAQ34780	Human adenosine re
17	1296.8	31.6	1310	21	AAQ34792	Human adenosine re
18	1296.8	31.6	146981	21	AAQ21442	Human ELAM-1 polyn
19	1280.8	31.2	1284	23	AB197987	Non-endogenous hum
20	1248.8	30.4	1284	23	AAQ63209	Human endothelin r
21	403.8	9.8	1965	13	AAQ25892	Sequence encodes e
22	399	9.7	4301	14	AAQ34584	ETb receptor gene
23	396.6	9.7	1406	15	AAQ53922	Bovine ET receptor
24	395.8	9.6	1632	24	AAQ24966	Human G-protein co
25	395.8	9.6	1719	21	AAQ21285	Human low adenosin
26	395.8	9.6	1720	21	AAQ35163	Human adenosine re
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30	395.8	9.6	4286	21	AAQ21284	Human low adenosin
31	395.8	9.6	4286	21	AAQ35162	Human adenosine re
32	395.8	9.6	13611	21	AAQ21288	Human low adenosin
33	395.8	9.6	13612	21	AAQ35166	Human adenosine re
34	392.6	9.6	1329	23	AB197988	Non-endogenous hum
35	383.2	9.3	1958	24	AB199321	Mouse ischaemic co
36	381.2	9.3	1578	21	AAQ21287	Human low adenosin
37	381.2	9.3	1578	21	AAQ35165	Human adenosine re
38	343	8.4	343	20	AAH87097	Human single nucle
39	284.4	6.9	438	24	ABL80342	Human ovarian canc
40	256.2	6.2	267	21	AAQ4557	Human secreted pro
41	255	6.2	255	19	AAQ11241	Human biallelic po
42	246.4	6.0	9118	24	ABQ66989	Human angiogenesis
43	246.4	6.0	9543	24	ABN80048	Human chemically m
44	243.6	5.9	9118	24	ABQ66990	Human angiogenesis
45	243.6	5.9	9543	24	ABN80049	Human chemically m

ALIGNMENTS

RESULT 1

AAQ34583

ID AAQ34583 standard; DNA; 4105 BP.

XX AAQ34583;

XX 11-MAY-1993 (first entry)

DE ETA receptor gene.

XX Human; ETA; ETb; endothelin; receptor; transmembrane domain; N tail;

XX extracellular; cytoplasmic; C tail; post translational; bovine;

XX modification; ET-1 receptor; antagonist; circulatory system; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 485..1768

FT sig_peptide /tag= a

FT mat_peptide /tag= b

FT polyA_signal /tag= c

FT misc_feature /tag= d

FT misc_feature /tag= e

FT misc_feature /function= Related with mRNA instability

FT misc_feature /tag= f

FT misc_feature /function= Related with mRNA instability

FT misc_feature 2309..2313

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FT FT /*tag= g
FT FT /function= Related with mRNA instability
FT FT 2386..2390
FT FT /*tag= h
FT FT /function= Related with mRNA instability
FT FT 2680..2684
FT FT /*tag= i
FT FT /function= Related with mRNA instability
FT FT 3252..3256
FT FT /*tag= j
FT FT /function= Related with mRNA instability
FT FT 3944..3948
FT FT /*tag= k
FT FT /function= Related with mRNA instability
XX
PN EP522868-A.
XX
XX 13-JAN-1993.
XX
XX 10-JUL-1992; 92EP-0306347.
XX
XX 12-JUL-1991; 91JP-0172828.
XX
PA (SHIO ) SHIONOGI SEIYAKU KK.
XX
XX Imura H, Nakanishi S, Nakao K;
XX
XX WPI; 1993-010677/02.
XX
XX P-PSDB; AAR30885.
XX
XX Human E7a and E7b endothelin receptors - for measuring endothelin
XX and screening for endothelin antagonists
XX
XX Claim 6; Fig 1; 39pp; English.
XX
XX The sequences given in AQ34593-84 encode the human E7a and E7b
XX endothelin receptors respectively. E7a is a 427 amino acid protein
XX with a molecular weight of 48,726. E7b comprises 442 amino acids and
XX has a molecular weight of 49,629. E7a has a higher affinity for
XX endothelin (ET)-1 and ET-2, whereas E7b has no selectivity for ET-1,
XX ET-2 or ET-3. The receptors each contain seven transmembrane domains
XX and have an extracellular N tail and a cytoplasmic C tail. There are
XX several potential sites for post translational modification, these
XX sites are identical to those of bovine ET-1 receptor. E7a cDNA is
XX 91.2% homologous to bovine ET-1 receptor cDNA and E7b cDNA is 61.1%
XX homologous to that of bovine E7a receptor. The receptor proteins are
XX useful as reagents for measuring the amount of ET or screening for
XX antagonists of the ET receptor when studying the circulatory system.
XX
XX Sequence 4105 BP; 1138 A; 860 G; 844 G; 1263 T; 0 other;

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Query Match 100.0%; Score 4103.4; DB 14; Length 4105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GAATTCGCGCGCGCTCTGCGGTCGCCAGAGTGGAGTGGAGGCTTGGAGGCTTGGAGG 60
Qy 61 AGACGGGAGGACAGACAGTGGAGGCGGTGTCTCCGAGCTTTCTTTTCGTCGAGCCCT 120
Db 61 AGACGGGAGGACAGACAGTGGAGGCGGTGTCTCCGAGCTTTCTTTTCGTCGAGCCCT 120
Qy 121 CGCGCGCGCTACAGTATCCGCTGGTCTGACGATTTGGAGGCGGTGGAGGCTT 180
Db 121 CGCGCGCGCTACAGTATCCGCTGGTCTGACGATTTGGAGGCGGTGGAGGCTT 180
Qy 181 CATCCATCCACCGCGTCTGCGCGGGATTGGGGTCCCGACACACCTCCCGGGAGAA 240
Db 181 CATCCATCCACCGCGTCTGCGCGGGATTGGGGTCCCGACACACCTCCCGGGAGAA 240
Qy 241 GCAGTGCACGAGAGTCTTCTGAAGCGGGGAAGCTGTGCAGCGGAAGCGCGCGCGC 300
Db 241 GCAGTGCACGAGAGTCTTCTGAAGCGGGGAAGCTGTGCAGCGGAAGCGCGCGCGC 300

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Db 241 GCAGTGCACGAGAGTCTTCTGAAGCGGGGAAGCTGTGCAGCGGAAGCGCGCGCGC 300
Qy 301 CGGAGCCCGGGACACCGCCACCTCCGCGGCACCCACCTCTCTCTCTCTCTCTCTCTCT 360
Db 301 CGGAGCCCGGGACACCGCCACCTCCGCGGCACCCACCTCTCTCTCTCTCTCTCTCTCT 360
Qy 361 TGGCCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 361 TGGCCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Qy 421 AAAAAAGTGAAGTGTAAAAAGTGAAGTGTAAAAAGTGAAGTGTAAAAAGTGAAGTGT 480
Db 421 AAAAAAGTGAAGTGTAAAAAGTGAAGTGTAAAAAGTGAAGTGTAAAAAGTGAAGTGT 480
Qy 481 CAAGATGGAAGCCCTTTTGGCTCAGGCGCATCTTTTGGCTCAGGCGCATCTTTTGGCT 540
Db 481 CAAGATGGAAGCCCTTTTGGCTCAGGCGCATCTTTTGGCTCAGGCGCATCTTTTGGCT 540
Qy 541 CAGTGATAATCTCTGAGAGATACAGCACAAATCTAAGCAATCATGTGATGATTTTCAACC 600
Db 541 CAGTGATAATCTCTGAGAGATACAGCACAAATCTAAGCAATCATGTGATGATTTTCAACC 600
Qy 601 TTTTCTGTCGACAGAGCTCAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660
Db 601 TTTTCTGTCGACAGAGCTCAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660
Qy 661 ACCCAGCAATGCTCAATGCACAACTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 720
Db 661 ACCCAGCAATGCTCAATGCACAACTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 720
Qy 721 CAAATACATTAACACTGTGATATCTTGTACTATTTTTCATCTGTTGTTGTTGTTGTTG 780
Db 721 CAAATACATTAACACTGTGATATCTTGTACTATTTTTCATCTGTTGTTGTTGTTGTTG 780
Qy 781 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCAACCGCTGAT 840
Db 781 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCAACCGCTGAT 840
Qy 841 AGCCAGTCTTGGCTTGGAGAGCTTATCTATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 900
Db 841 AGCCAGTCTTGGCTTGGAGAGCTTATCTATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 900
Qy 901 TAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 TAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy 961 GCTGTTCCCTTTTTCGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 GCTGTTCCCTTTTTCGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Qy 1021 TAGTCTTGACAGTACAGAGAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1021 TAGTCTTGACAGTACAGAGAGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Qy 1081 TTTGTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 TTTGTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 1141 TGAAGCGATTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 TGAAGCGATTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Qy 1201 TATGCTCAATGCCACATCAAAATTCATGAGTTCTTACCAAGATGTAAAGGACTTGGTGG 1260
Db 1201 TATGCTCAATGCCACATCAAAATTCATGAGTTCTTACCAAGATGTAAAGGACTTGGTGG 1260
Qy 1261 CTTTGGGTTCTATTTCTGTATGCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1261 CTTTGGGTTCTATTTCTGTATGCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Qy 1321 TTGTGAGATGTTGAACAGAGGAATGGCAGCTTGAAGATTTGCCCTCAGTGAACATCTTAA 1380
Db 1321 TTGTGAGATGTTGAACAGAGGAATGGCAGCTTGAAGATTTGCCCTCAGTGAACATCTTAA 1380

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QY	1381	GCAGCGT	CGAGAA	GTGCGCAAAACACGCTTTTCTGCTTGGTGTGTAATTTTGTGCTCTTTGCTG	1440
DB	1381	GCAGCGT	CGAGAA	GTGCGCAAAACACGCTTTTCTGCTTGGTGTGTAATTTTGTGCTCTTTGCTG	1440
QY	1441	GTTCCCT	CTCTCACTTAAAGCCGTATATTGAAGAAAACCTGTATACCGAAATGACAAGAA	1500	
DB	1441	GTTCCCT	CTCTCACTTAAAGCCGTATATTGAAGAAAACCTGTATACCGAAATGACAAGAA	1500	
QY	1501	CCGATGT	GAAATTA	CTTACTGCTCATGGAATACATCGGTAATTAACATTTGCAAC	1560
DB	1501	CCGATGT	GAAATTA	CTTACTGCTCATGGAATACATCGGTAATTAACATTTGCAAC	1560
QY	1561	CATGAAT	TCATCTATAAACCCCATAGCTCTGTATTTTGTGACGACAAATTTAAAATTC	1620	
DB	1561	CATGAAT	TCATCTATAAACCCCATAGCTCTGTATTTTGTGACGACAAATTTAAAATTC	1620	
QY	1621	TTTCCAGT	CATCCCTCTGCTGCTGTATACCAGTCCAAAAGTCTGATGACCTCGGTC	1680	
DB	1621	TTTCCAGT	CATCCCTCTGCTGCTGTATACCAGTCCAAAAGTCTGATGACCTCGGTC	1680	
QY	1681	CATGAC	GGAACAAGCATCCAGTGGAAAGAACACGATCAAAACACACGACG	1740	
DB	1681	CATGAC	GGAACAAGCATCCAGTGGAAAGAACACGATCAAAACACACGACG	1740	
QY	1741	GAGCAG	CCATTAAGGACAGCATCACTGACACCCCTTAGAGCACCTCTCGGTACTCCCAT	1800	
DB	1741	GAGCAG	CCATTAAGGACAGCATCACTGACACCCCTTAGAGCACCTCTCGGTACTCCCAT	1800	
QY	1801	AATCCT	CTCGGAGAAAAAATCACAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860	
DB	1801	AATCCT	CTCGGAGAAAAAATCACAGGCAACTGTGACTCCGGGAATCTTCTCTGATC	1860	
QY	1861	CTTCT	CTCTTAATTCACCTCCACACCCCAAGAGAAATGCTTCCAAAACCGCAAGTAGA	1920	
DB	1861	CTTCT	CTCTTAATTCACCTCCACACCCCAAGAGAAATGCTTCCAAAACCGCAAGTAGA	1920	
QY	1921	CTGGT	TTATCCACCCACACATCTAGGAATCGTACTCTTAAATGATCTAATTTACATA	1980	
DB	1921	CTGGT	TTATCCACCCACACATCTAGGAATCGTACTCTTAAATGATCTAATTTACATA	1980	
QY	1981	TTCTCG	TGTGTATTCAGCACATAAAATGGTGGGAGCTGGGGAGAAATGAAGACTGT	2040	
DB	1981	TTCTCG	TGTGTATTCAGCACATAAAATGGTGGGAGCTGGGGAGAAATGAAGACTGT	2040	
QY	2041	AAATGAA	ACCAGAGGATTTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGG	2100	
DB	2041	AAATGAA	ACCAGAGGATTTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATGG	2100	
QY	2101	CTAGCT	TTTATGGCAGTCTGGTGAATGTTCAATGGGAACCTGGTCAACCATGAACCTTTAG	2160	
DB	2101	CTAGCT	TTTATGGCAGTCTGGTGAATGTTCAATGGGAACCTGGTCAACCATGAACCTTTAG	2160	
QY	2161	AGATTAA	CGACAAAGATTTTCTACTTTTAAAGTGATTTTGTCTCCTCAGCAACACACA	2220	
DB	2161	AGATTAA	CGACAAAGATTTTCTACTTTTAAAGTGATTTTGTCTCCTCAGCAACACACA	2220	
QY	2221	ATATGG	CTCAGGTCACGTCACATTTATTTGAAATGTCATTTGGTCCAGTATTTTAACTGCA	2280	
DB	2221	ATATGG	CTCAGGTCACGTCACATTTATTTGAAATGTCATTTGGTCCAGTATTTTAACTGCA	2280	
QY	2281	TAATAG	CCTAACATGATTTTGAACCTATTTTACACATAGTTTGAAAAAAGACAAA	2340	
DB	2281	TAATAG	CCTAACATGATTTTGAACCTATTTTACACATAGTTTGAAAAAAGACAAA	2340	
QY	2341	AATAGT	ATTCAGGTGAGCAATTAGATATTTTCCAGCTCACATTTATTTTAAAA	2400	
DB	2341	AATAGT	ATTCAGGTGAGCAATTAGATATTTTCCAGCTCACATTTATTTTAAAA	2400	
QY	2401	ACACAAA	TTCTAAAGCTACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460	
DB	2401	ACACAAA	TTCTAAAGCTACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460	

Qy	2461	TTTGGCAGTTTAAATAGATGTTTACTCAAGAATTTTTTAAAGAACGTATTTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTTACTCAAGAATTTTTTAAAGAACGTATTTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTGTATGTTAAATTCAAAAGTAATGC	2580
Db	2521	ATGGTGTTTTATTACAAGGGACCTTGAACATGTTTGTATGTTAAATTCAAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAAATACTGTTTTTCATGTAAATTTTTGTATGA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAAATACTGTTTTTCATGTAAATTTTTGTATGA	2640
Qy	2641	AAATCAATGCAAGTACCAAAATGTTAAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Db	2641	AAATCAATGCAAGTACCAAAATGTTAAATGTATGTGTCAATTTAACTCTGCCTGAGACTT	2700
Qy	2701	TCAGTGCACCTGTATAGAACTTAAACACACACTTAAGAGAAAAGATCGAATTTTTTCAG	2760
Db	2701	TCAGTGCACCTGTATAGAACTTAAACACACACTTAAGAGAAAAGATCGAATTTTTTCAG	2760
Qy	2761	ATGATTCGGAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Db	2761	ATGATTCGGAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATAT	2820
Qy	2821	CACCTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGTATCA	2880
Db	2821	CACCTCCTATTCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTTTGTATCA	2880
Qy	2881	TTCCCTTTTCCATATAGAGAAACATAATTTTGAAGTGCCAGATGAGTTTATCATGTGCTGT	2940
Db	2881	TTCCCTTTTCCATATAGAGAAACATAATTTTGAAGTGCCAGATGAGTTTATCATGTGCTGT	2940
Qy	2941	GAAAAATAATTACCCACAAAATGCCACCAGTAACATTAACGATTCCTTCACCTCTCTGGGGTTT	3000
Db	2941	GAAAAATAATTACCCACAAAATGCCACCAGTAACATTAACGATTCCTTCACCTCTCTGGGGTTT	3000
Qy	3001	TCAGTATGAACCTTAACCTCCCAACCAACATCTCCCTCCCAATTTGTCACCAATTTCAAAG	3060
Db	3001	TCAGTATGAACCTTAACCTCCCAACCAACATCTCCCTCCCAATTTGTCACCAATTTCAAAG	3060
Qy	3061	GGCCACAGTGACTTTGGCTGGGCATTTTCCACATGTTTACAGACGTGTGAGTACACGAG	3120
Db	3061	GGCCACAGTGACTTTGGCTGGGCATTTTCCACATGTTTACAGACGTGTGAGTACACGAG	3120
Qy	3121	AAAACTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTATGCC	3180
Db	3121	AAAACTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTATGCC	3180
Qy	3181	ATTTTCTPAGACTCTCTGTGGAATATATTGTGTGTGATATATGATGTGTGTGAT	3240
Db	3181	ATTTTCTPAGACTCTCTGTGGAATATATTGTGTGTGATATATGATGTGTGTGAT	3240
Qy	3241	GGTATGATGATTTAATCTAATTAATTTGTCCTCCGAGTTGTGGCCAAAGTGATTA	3300
Db	3241	GGTATGATGATTTAATCTAATTAATTTGTCCTCCGAGTTGTGGCCAAAGTGATTA	3300
Qy	3301	GTCGAGCTAAAATCTAGGTGATTTGTCATCATGACAACTGCTCAGTCCATTTTAAAC	3360
Db	3301	GTCGAGCTAAAATCTAGGTGATTTGTCATCATGACAACTGCTCAGTCCATTTTAAAC	3360
Qy	3361	TGTAGCAACCTTCTGCATTCATAATCTTGTAAATGTTTACCAATTAACAATGGGATATA	3420
Db	3361	TGTAGCAACCTTCTGCATTCATAATCTTGTAAATGTTTACCAATTAACAATGGGATATA	3420
Qy	3421	AGAGCAGCGTGAAGCAGATGAGCTGTGGACATGATAGGGTTTGTGGTGGT	3480
Db	3421	AGAGCAGCGTGAAGCAGATGAGCTGTGGACATGATAGGGTTTGTGGTGGT	3480
Qy	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTTGTTCCCTGTGCTGGAGCAAAAGTCATTA	3540
Db	3481	TGGTTTGATAAAGCAGTATTTGGGGTCATATTTGTTCCCTGTGCTGGAGCAAAAGTCATTA	3540
Qy	3541	CACTTTGAAGTATTTATTTGTTCTTATCCCTCAATTTCAATGTGGTGATGAAATTTGCCAGGT	3600

Db	3541	CAC	TTTGAGTATTATATGTTCTTATCCTCAATTCATGTTGGTATGAATAATGCCAGGT	3600
Qy	3601	TG	CTGATATTCTTTCAGACTTTCGCCACACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Db	3601	TG	CTGATATTCTTTCAGACTTTCGCCACACAGATTGCTGATAATAAAATTAGGTAAGATA	3660
Qy	3661	ATT	TGTTGGGCCATATTTTAGACAGAGTAAATAACATCAGGTTCCAGTTCGCTTGAATTG	3720
Db	3661	ATT	TGTTGGGCCATATTTTAGGACAGGTAATAACATCAGGTTCCAGTTCGCTTGAATTG	3720
Qy	3721	CA	GGCTTAAGAAGTACTGGCCCTTTTGTTGTAGCAGTCAAAATCTATTATTTCCACTCGCG	3780
Db	3721	CA	GGCTTAAGAAGTACTGGCCCTTTTGTTGTAGCAGTCAAAATCTATTATTTCCACTCGCG	3780
Qy	3781	CA	TATATGCAGTGATATATGCGTATATATTAAGCCATAGGTTCCACACCATTTGTTTATG	3840
Db	3781	CA	TATATGCAGTGATATATGCGTATATATTAAGCCATAGGTTCCACACCATTTGTTTATG	3840
Qy	3841	ACA	ATTGCTCTTTTTTTTCAAGATGCTTTGTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Db	3841	ACA	ATTGCTCTTTTTTTTCAAGATGCTTTGTTCTTTCATATGAAAAAATGCATTTTATAA	3900
Qy	3901	ATT	CAGAAAGTCATAGATTCTTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAAG	3960
Db	3901	ATT	CAGAAAGTCATAGATTCTTGAAGGCGTCAACGTGCATTTTATTTATGGACTGGTAAAG	3960
Qy	3961	TAA	CTGTGGTTTACTAGCAGGAATATTTCCAAATTTCTACCTTTTACTACATCTTTTCAACA	4020
Db	3961	TAA	CTGTGGTTTACTAGCAGGAATATTTCCAAATTTCTACCTTTTACTACATCTTTTCAACA	4020
Qy	4021	AG	TAACTTTCTAGAAATGAGCCAGAGGCGCAAGGCCCTCGAGTTGGCAGTGGCCCATAGTG	4080
Db	4021	AG	TAACTTTCTAGAAATGAGCCAGAGGCGCAAGGCCCTCGAGTTGGCAGTGGCCCATAGTG	4080
Qy	4081	TAAA	ATAAAGTTTACAGAAACCTT	4105
Db	4081	TAAA	ATAAAGTTTACAGAAACCTT	4105

RESULT 2

RESOL 2
AAA38341
ID AAA38341 standard; DNA: 4105 BP.

AC AAA38341:

DT 21-AUG-2000 (first entry)

Human endothelin receptor type A gene coding region.

Endothelin receptor type A gene; coding region:

...
KW
KW
KW

OS Homo sapiens.

PN WO200022166-A2.

XX
PD
20-APR-2000

XX
PF
13-OCT-1999: 99WQ-TB01678

XX
PR 14-OCT-1998; 98US-0104286.

PR 14-OCT-1998; 98US-0104302.

PA (EURO-) EURONA MEDICAL AB.

PI Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;

XX
DR WPI; 2000-318010/27.

[illegible]

PT Assessing cardiovascular status in humans involves comparing test

polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern -

Disclosure; Page 125-126; 126pp: English.

The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen. Fragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or eliminates trial and error in selecting a treatment for a particular individual cardiovascular patient. It also provides the ability to eliminate patients from clinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular treatment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be correlated with a sub-population of the test population, permitting exclusion of such sub-populations from the treatment group. Beneficial drugs can be approved for use in the appropriate population, thereby decreasing the number of patients required for a clinical trial, which in turn decreases the duration and cost of such trials. The present sequence represents the human endothelin receptor type A gene coding region (GenBank S57498). The polymorphic sites identified are 969C/T, 1005A/G, 1146A/G and 2485T/C.

SQ Sequence 4105 BP; 1138 A; 859 C; 843 G; 1263 T; 2 other;

Query Match 100.0%; Score 4103; DB 21; Length 4105;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 4103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTCCGGCGCGCCTCTTTCGGGTCCCAGAGTGGAGTGGAGGCTCTGGAGCTTTGGGAGG 60

Db 1 GAATTCCGGGGCGGCTCTTTCGGTCCACAGTCCAGTGGAGTGAAGTCTGGAGCTTGGGAGG 60

QY 61 AGACGGGGAGGACAGACTGGAGGCGTCTTCCCTCCGGAGTCTTTCTTTTTCGTGCGAGCCCT 120

Db 61 AGACGGGAGGACAGACTGGAGGCGTTCTCCGGAGTTTCTTTTCGTGCGAGCCCT 120

QY 121 CGCGCGCGGTACAGTCAATCCCGCTGGTCTGACGATTCTGGAGAGCGCGGTGGAGAGGCTT 180

Db 121 CGCGCGCGGTACAGTCATCCCGCTGCTGACGATTGTGGAGAGGCGGTTGGAGAGGCTT 180

QY 181 CATCCATCCACCCGGTGGTTCGCCGGGGATGGGGTCCACGACACCTCCCCCGGGAGAA 240

LD
101 CATCCCTTCCCACCCCCCGTCGTCGCCCGGGGAAITGGGGGTCCCCAGCAGCACATCCCCCCGGGGAGAA 24

241

0v 301 CGGAGCCCGGGCACAACCGGCCAACCTTCGCGCCCAACCCACCTTCCATTTCTTC 360

Db 301 CGGAGCCCGGACACCGGCCACCCCTCGCGCCA CCCACCGCGCTTCTCGGGTTCCTC 360

Qy	361	TGGCCCAAGCGCCGCGCGGACCGCGAGCTGTCTGCGCAGCCGCGACTCCACGGTGA AAAA	420
Db	361	TGGCCCAAGCGCGCGCGGACCGCGAGCTGTCTGCGCAGCCGCGACTCCACGGTGA AAAA	420
Qy	421	AAAAAGTGAAGGTGTA AAAAGCAGCAAGTGCAATAAGAGATATTTCCCTCAAAATTTGCCT	480
Db	421	AAAAAGTGAAGGTGTA AAAAGCAGCAAGTGCAATAAGAGATATTTCCCTCAAAATTTGCCT	480
Qy	481	CAAGATGAAACCCCTTTGGCCTCAGGCGATCCCTTTTGGCTGGCAGCTGGTGTGGATGTGTAAT	540
Db	481	CAAGATGAAACCCCTTTGGCCTCAGGCGATCCCTTTTGGCTGGCAGCTGGTGTGGATGTGTAAT	540
Qy	541	CAGTGATAATCCTGAGAGATACAGCACAATACTTAAGCAATCATGTGGATGATTTCAACAC	600
Db	541	CAGTGATAATCCTGAGAGATACAGCACAATACTTAAGCAATCATGTGGATGATTTCAACAC	600
Qy	601	TTTTTCGTGGCAGAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACCTAAATTTGGTTCCT	660
Db	601	TTTTTCGTGGCAGAGAGCTCAGCTTCCTGGTTACCACTCATCAACCCACCTAAATTTGGTTCCT	660
Qy	661	ACCCAGCAATGGCTCAATGCACAACTATTTGCCACAGCAGACTAAATTTACTTCAGCTTT	720
Db	661	ACCCAGCAATGGCTCAATGCACAACTATTTGCCACAGCAGACTAAATTTACTTCAGCTTT	720
Qy	721	CAAAATACATTAACACTGTGATATCTTTACTATTTTTCATCTGTGGAAATGGTGGGGAATGC	780
Db	721	CAAAATACATTAACACTGTGATATCTTTACTATTTTTCATCTGTGGAAATGGTGGGGAATGC	780
Qy	781	AACCTCTGCTCAGGATCATTTACAGAACAAATGTATGAGGAATGGCCCCAACGGGCTGAT	840
Db	781	AACCTCTGCTCAGGATCATTTACAGAACAAATGTATGAGGAATGGCCCCAACGGGCTGAT	840
Qy	841	AGCCAGCTTTGCCCTTGGAGACCTTATCTATGTGGTCAITGATCTCCCTNTCAATGTATT	900
Db	841	AGCCAGCTTTGCCCTTGGAGACCTTATCTATGTGGTCAITGATCTCCCTNTCAATGTATT	900
Qy	901	TAAGCTCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA	960
Db	901	TAAGCTCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA	960
Qy	961	CTGTCTCCCTTTTTCGAGAAATGCTCGGTGGGATACCGCTCTCAACCTCTCGGCTCT	1020
Db	961	CTGTCTCCCTTTTTCGAGAAATGCTCGGTGGGATACCGCTCTCAACCTCTCGGCTCT	1020
Qy	1021	TAGTGTTCAGAGTACAGAGCAGTTCGCTTCCTGGAGTCGTCTCAGGAAATGGGATTC	1080
Db	1021	TAGTGTTCAGAGTACAGAGCAGTTCGCTTCCTGGAGTCGTCTCAGGAAATGGGATTC	1080
Qy	1081	TTTGGTAACTGCCATTGAAATTTGCTCCATCTCGATCTGCTCTTTATCCTGGCCATTCC	1140
Db	1081	TTTGGTAACTGCCATTGAAATTTGCTCCATCTCGATCTGCTCTTTATCCTGGCCATTCC	1140
Qy	1141	TGAAGCATTTGGCTTCGTATGTTACCTTTCGAATATAGGGGTGAACAGATATAAACCTG	1200
Db	1141	TGAAGCATTTGGCTTCGTATGTTACCTTTCGAATATAGGGGTGAACAGATATAAACCTG	1200
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Db	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCT	1260
Qy	1261	CTTCGGGTCTATTTCTGATGCCCTTGGTGTGCATCGATCTTCTACACCCCTCATGAC	1320
Db	1261	CTTCGGGTCTATTTCTGATGCCCTTGGTGTGCATCGATCTTCTACACCCCTCATGAC	1320
Qy	1321	TTGTGAGATGTTCAACAGAAAGAAATGGCAGCTTGAGAAATTCGCTCAGTGAACATCTTAA	1380
Db	1321	TTGTGAGATGTTCAACAGAAAGAAATGGCAGCTTGAGAAATTCGCTCAGTGAACATCTTAA	1380
Qy	1381	GCAGCGTCGAGAAATGGCAAAACAGTTTCTTCGTTCGCTGCTTAATTTTTCCTTCCTGCTG	1440
Db	1381	GCAGCGTCGAGAAATGGCAAAACAGTTTCTTCGTTCGCTGCTTAATTTTTCCTTCCTGCTG	1440
Qy	1441	GTTCCTCTCTTACTTAAGCCGTATATTGAAGAAAACTGTGTATAACGAAATGGCAAGAA	1500

Db	1441	 GTTCCCTCTTCACTTAAGCGGTATTTGAAGAAAACTGTGTATAAGCAAAATGACACAAGAA	1500
Qy	1501	CCGATCGTAATTACTTAGTGTTCCTACTGCTCATGGATATACATCGGTATTAACCTTGCGCAAC	1560
Db	1501	CCGATCGTAATTACTTAGTGTTCCTACTGCTCATGGATATACATCGGTATTAACCTTGCGCAAC	1560
Qy	1561	CATGAATTCATGATATAAACCCCATAGCTCTGTATTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	1561	CATGAATTCATGATATAAACCCCATAGCTCTGTATTTGTGAGCAAGAAATTTAAAAATTG	1620
Qy	1621	TTTCCAGTCATGCGCTCTGCTGCTGTGTACACAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1621	TTTCCAGTCATGCGCTCTGCTGCTGTGTACACAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Qy	1681	CATGAACGGAACNAGCATCCAGTGGGAAGAACACAGCATCAAAACACCAACACACACCG	1740
Db	1681	CATGAACGGAACNAGCATCCAGTGGGAAGAACACAGCATCAAAACACCAACACACACCG	1740
Qy	1741	GAGCAGCCATAAGGACAGCATGAACGTACACCCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1741	GAGCAGCCATAAGGACAGCATGAACGTACACCCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTCTCTGATC	1860
Db	1801	AATCCTCTCGGAGAAAAAATCACAAGGCAACTGTGACTCCGGGAATCTCTCTCTGATC	1860
Qy	1861	CTTCTTCTTAATTCCTACTCCACACCCAGAAGAAATGCTTCCAAAACCGCAAGTAGA	1920
Db	1861	CTTCTTCTTAATTCCTACTCCACACCCAGAAGAAATGCTTCCAAAACCGCAAGTAGA	1920
Qy	1921	CTGGTTTATCCACCCACAACATCTAGAACTCGTACTTCCTTAATTCATTAATTTACATA	1980
Db	1921	CTGGTTTATCCACCCACAACATCTAGAACTCGTACTTCCTTAATTCATTAATTTACATA	1980
Qy	1981	TTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Db	1981	TTCTGCGTGTGTATTTCAGCACTAAAAAATGGTGGGAGCTGGGGGAGAATGAAGACTGTT	2040
Qy	2041	AAATGAACACGAGGATTAATTTACTACTTTTGCATGAAATAGAGCTTTCAGTACATGG	2100
Db	2041	AAATGAACACGAGGATTAATTTACTACTTTTGCATGAAATAGAGCTTTCAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTCTGTGGTAATGTTCAATGGAACTGGTCAACCATGAACCTTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTCTGTGGTAATGTTCAATGGAACTGGTCAACCATGAACCTTTAG	2160
Qy	2161	AGATTAAACGACAAGATTTTCTACTTTTTTAAAGTGATTTTTTGTCCCTTCAGGCCAAACACA	2220
Db	2161	AGATTAAACGACAAGATTTTCTACTTTTTTAAAGTGATTTTTTGTCCCTTCAGGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACTTTTATTTGAATGTCATTTGGTGGCAGTATTTTTTAAGTGA	2280
Db	2221	ATATGGGCTCAGGTCACTTTTATTTGAATGTCATTTGGTGGCAGTATTTTTTAAGTGA	2280
Qy	2281	TAATAGCCTTAACATGATTAATTTGAACTTATTTACATAGTTTGAAGAAAAAAGACAAA	2340
Db	2281	TAATAGCCTTAACATGATTAATTTGAACTTATTTACATAGTTTGAAGAAAAAAGACAAA	2340
Qy	2341	AAATAGTATTCAGGTGAGCAATTAGATTTATTTTCCAGCTCAGTATTTTATTTTAAA	2400
Db	2341	AAATAGTATTCAGGTGAGCAATTAGATTTATTTTCCAGCTCAGTATTTTATTTTAAA	2400
Qy	2401	ACACAAATTCFAAGCTCAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTCFAAGCTCAACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATGTTTACTCAAAGAAATTTTTTAAAGAACTGATTTATTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATGTTTACTCAAAGAAATTTTTTAAAGAACTGATTTATTTTAA	2520
Qy	2521	ATGGTGTTTTATTAACAAGGACCTTTGAACATGTTTGTATGTTAAATTCAAAAGTAATGC	2580

Db 2521 ATGGTGTATTTTACAAAGGACCTTGAACATGTTTGTATGTTAAATTCAAAAGTAATGC 2580
 Qy 2581 TTCAATCAGATAGTCTTTTTCACAAAGTTCAATPACTGTTTTCATCATGTAATTTTGTATGA 2640
 Db 2581 TTCAATCAGATAGTCTTTTTCACAAAGTTCAATPACTGTTTTCATCATGTAATTTTGTATGA 2640
 Qy 2641 AAAATCAATGTCAAAGTACCAAAATGTTAATGATGTTGTCATTAACTCTGCCGTGAGACTT 2700
 Db 2641 AAAATCAATGTCAAAGTACCAAAATGTTAATGATGTTGTCATTAACTCTGCCGTGAGACTT 2700
 Qy 2701 TCAGTGCACTGTATATAGAAAGTCTAAACACACACCTTAAGAGAAAAAGATCGAATTTTTCAG 2760
 Db 2701 TCAGTGCACTGTATATAGAAAGTCTAAACACACACCTTAAGAGAAAAAGATCGAATTTTTCAG 2760
 Qy 2761 ATGATTCGGAATTTTCATTCAGGATTTTGTAAATAGTAGACATATATATATATACATAT 2820
 Db 2761 ATGATTCGGAATTTTCATTCAGGATTTTGTAAATAGTAGACATATATATATATACATAT 2820
 Qy 2821 CACCTCCCTATCTCTTAATTTTGTAAATAGTAGAGTAACTGGCAGTAAGTCTTTTGTGATCA 2880
 Db 2821 CACCTCCCTATCTCTTAATTTTGTAAATAGTAGAGTAACTGGCAGTAAGTCTTTTGTGATCA 2880
 Qy 2881 TTCCTCTTTTCCATATAGGAACATATTTGAAGTGGCCAGATGAGTTTATCATGTCACT 2940
 Db 2881 TTCCTCTTTTCCATATAGGAACATATTTGAAGTGGCCAGATGAGTTTATCATGTCACT 2940
 Qy 2941 GAAAAATAATTAACCCACAAATGCCACCACTAACTTAACGATCTTCACATCTTTGGGGTTT 3000
 Db 2941 GAAAAATAATTAACCCACAAATGCCACCACTAACTTAACGATCTTCACATCTTTGGGGTTT 3000
 Qy 3001 TCAGTATGAACCTAACTCCCCACCCACACATCTCCCTCCACATGTGCCAATTTTCAAG 3060
 Db 3001 TCAGTATGAACCTAACTCCCCACCCACACATCTCCCTCCACATGTGCCAATTTTCAAG 3060
 Qy 3061 GGCCACAGTACTTTTGTGGGCAATTTCCACAGATGTTTACAGAGTGTGACGTACAGCAG 3120
 Db 3061 GGCCACAGTACTTTTGTGGGCAATTTCCACAGATGTTTACAGAGTGTGACGTACAGCAG 3120
 Qy 3121 AAAATCTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTAGCC 3180
 Db 3121 AAAATCTTTTACTAGTGTGTGTATATATAAACAATTTGTAATTTCTTTTAGCC 3180
 Qy 3181 ATTTTCTAGACTGCTCTGGGAATATATTGTGTGTGTGTATATATGATGTGTGTAT 3240
 Db 3181 ATTTTCTAGACTGCTCTGGGAATATATTGTGTGTGTGTATATATGATGTGTGTAT 3240
 Qy 3241 GGTATGTATGATTAATCTAATCTAATTAATTTGCCCGCAGTTGTGCCAAGTGCATA 3300
 Db 3241 GGTATGTATGATTAATCTAATCTAATTAATTTGCCCGCAGTTGTGCCAAGTGCATA 3300
 Qy 3301 GTCTGAGCTAAATCTAGGTGATTTCTCATCATGACAACCTGCCCTCAGTCCATTTTAACC 3360
 Db 3301 GTCTGAGCTAAATCTAGGTGATTTCTCATCATGACAACCTGCCCTCAGTCCATTTTAACC 3360
 Qy 3361 TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTTACAAATGGGATATA 3420
 Db 3361 TGTAGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTTACCATTTACAAATGGGATATA 3420
 Qy 3421 AGAGCAGCGTGAAGCAGATGAGCTGTGGACTACATATAGGGTTTGTGTTGGT 3480
 Db 3421 AGAGCAGCGTGAAGCAGATGAGCTGTGGACTACATATAGGGTTTGTGTTGGT 3480
 Qy 3481 TGGTTTGTAAAGCAGATTTTGGGGTCAATTTGTTCTGCTGCTGAGCAAAAGTCATTA 3540
 Db 3481 TGGTTTGTAAAGCAGATTTTGGGGTCAATTTGTTCTGCTGCTGAGCAAAAGTCATTA 3540
 Qy 3541 CACTTTGAAGTATATATGTTCTTATCTCAATTCATGTTGGTGTATGAAATGGCCAGT 3600
 Db 3541 CACTTTGAAGTATATATGTTCTTATCTCAATTCATGTTGGTGTATGAAATGGCCAGT 3600
 Qy 3601 TGTCTGATATTTCTTTCAGACTTCGCCACAGAGATGCTGATATAAATTAGTGAAGATA 3660
 Db 3601 TGTCTGATATTTCTTTCAGACTTCGCCACAGAGATGCTGATATAAATTAGTGAAGATA 3660

RESULT 3

AAAL39858
 ID AAL39858 standard; DNA; 2595 BP.

XX AC AAL39858;

XX XX 05-SEP-2002 (first entry)

XX DE Human allergy-associated gene SEQ ID No 30.

XX KW Antiallergic; allergic disease; carboxypeptidase M; cathepsin C; CYP1B1;
 KW endoserine A receptor; osteoblast-specific factor 2; DD96; gene therapy;
 KW bronchial asthma; human; ds.

XX OS Homo sapiens.

XX PN WO200252006-A1.

XX XX 04-JUL-2002.

XX PF 21-DEC-2001; 2001WO-JP11287.

XX PR 26-DEC-2000; 2000JP-0396166.

XX XX (GENO-) GENOX RES INC.

XX PI Ohtani N, Matsui K, Yoshida N, Sugita Y, Izuhara K;

XX DR WPI; 2002-500763/53.

XX PT Examining allergic diseases by changes in expression levels of six
 PT allergy-associated genes inducible by stimulation e.g. of airway
 PT epithelial cells with interleukin-4 or 13, also applicable in screening
 compounds

XX PS Disclosure; Page 79-80; 106pp; Japanese.

XX CC The invention relates to a novel method for examining allergic diseases,
 comprising determining the expression level of a gene selected from

CC carboxypeptidase M, cathepsin C, endoserine A receptor, osteoblast-specific factor 2, DP96 and CYP1B1 in the biological sample from a patient, and comparing the expression level with that in the sample of a healthy individual. The polynucleotides of the invention can be used to treat disorders by gene therapy. The method is useful for examining allergic diseases particularly bronchial asthma and its diagnosis, which is also applicable in screening candidate compounds for remedies. This polynucleotide sequence represents a human allergy-associated gene of the invention.

XX Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 other;

Query Match		60.2%	Score 2470;	DB 24;	Length 2595;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 2481; Conservative		0;	Mismatches	0;	Indels 1; Gaps 1;
QY	1624	CCAGTCATGCCCTCTGCTGCTGTGTACAGTCCAAAAGTCTGTAGACCTCGGTCCCCAT	1683		
b	15	CCAGTCATGCCCTCTGCTGCTGTGTACAGTCCAAAAGTCTGTAGACCTCGGTCCCCAT	74		
QY	1684	GAACGGAACAGCATCCAGTGAAGAACACACGATCAAAACACCAACAGACCGGAG	1743		
Db	75	GAACGGAACAGCATCCAGTGAAGAACACACGATCAAAACACCAACAGACCGGAG	134		
QY	1744	CAGCCATAAGGACAGCATGAAGTACACCCCTTAGAAGCACTCCCGTACTCCCATAT	1803		
Db	135	CAGCCATAAGGACAGCATGAAGTACACCCCTTAGAAGCACTCCCGTACTCCCATAT	194		
QY	1804	CCTCTCGGAGAAAAAATCACAAGCAACTGTGACTCCGGGAATCTCTCTGATCCCT	1863		
Db	195	CCTCTCGGAGAAAAAATCACAAGCAACTGTGACTCCGGGAATCTCTCTGATCCCT	254		
QY	1864	CTTCTTAATTCACCTCCACACCCCAAGAAAGTCTTTCCAAAACCGCAAGTAGACTG	1923		
Db	255	CTTCTTAATTCACCTCCACACCCCAAGAAAGTCTTTCCAAAACCGCAAGTAGACTG	314		
QY	1924	GTTTATCCACCACCAACATCTACGAATCGTACTCTTTAAATGATCTAATTTACATATTC	1983		
Db	315	GTTTATCCACCACCAACATCTACGAATCGTACTCTTTAAATGATCTAATTTACATATTC	374		
QY	1984	TGCGTGTGTATTCAGCACTAAAATGCTGGGAGCTGGGGAGAAATGAAGACTGTTAA	2043		
Db	375	TGCGTGTGTATTCAGCACTAAAATGCTGGGAGCTGGGGAGAAATGAAGACTGTTAA	434		
QY	2044	TGAACACCAAGAGGATATTTACTACTTTTCATGAAATAGAGCTTTCAGTACATGGCTA	2103		
b	435	TGAACACCAAGAGGATATTTACTACTTTTCATGAAATAGAGCTTTCAGTACATGGCTA	494		
QY	2104	GCTTTTATGGCAGTCTGGTGAATGTTCAATGGGAACCTGGTCAACATGAACTTTAGAGA	2163		
Db	495	GCTTTTATGGCAGTCTGGTGAATGTTCAATGGGAACCTGGTCAACATGAACTTTAGAGA	554		
QY	2164	TTAAGCACAAGATTTCTACTTTTAAAGTGATTTTTCCTTCAGCCAAACAATA	2223		
Db	555	TTAAGCACAAGATTTCTACTTTTAAAGTGATTTTTCCTTCAGCCAAACAATA	614		
QY	2224	TGGGCTCAGGTCACCTTTATTTGAAATGCTCAATTTGGTGCCAGTATTTTAACTGCTATA	2283		
Db	615	TGGGCTCAGGTCACCTTTATTTGAAATGCTCAATTTGGTGCCAGTATTTTAACTGCTATA	674		
QY	2284	TAGCCTAACATGATTTTGAACCTTATTTACACATAGTTTGAACAAAAAAGACAAAAAT	2343		
Db	675	TAGCCTAACATGATTTTGAACCTTATTTACACATAGTTTGAACAAAAAAGACAAAAAT	734		
QY	2344	AGTATTCAGGTGAGCAATAGATAGTATTTTCCACGTCACCTATTTTAAAAACA	2403		
Db	735	AGTATTCAGGTGAGCAATAGATAGTATTTTCCACGTCACCTATTTTAAAAACA	794		
QY	2404	CAAAATCTAAGCTACACAAATFACTACAGCCCTTTAAAGCACAGTCTGATGACACATTT	2463		
Db	795	CAAAATCTAAGCTACACAAATFACTACAGCCCTTTAAAGCACAGTCTGATGACACATTT	854		
QY	2464	GGCAGTTTAAATAGTGTACTCAAGAAATTTTAAAGAACTGTATTTTAAATG	2523		

Db	855	GGCAGTTTAAATAGTGTACTCAAGAAATTTTAAAGAACTGTATTTTAAATG	914		
QY	2524	GTCTTTTATACAGGACCTTGAACATGTTTGTATGTTAAATCAAAAGTAAATGCTTC	2583		
Db	915	GTCTTTTATACAGGACCTTGAACATGTTTGTATGTTAAATCAAAAGTAAATGCTTC	974		
QY	2584	AATCAGATAGTCTCTTTTCAACAGTTCACATCTGTTTTTTCATGTAATTTTGTATGAAA	2643		
Db	975	AATCAGATAGTCTCTTTTCAACAGTTCACATCTGTTTTTTCATGTAATTTTGTATGAAA	1033		
QY	2644	ATCAATGTCAAGTACCAAAATGTTAATGTTGTTCAATTTAACTCTCCCTGAGACTTCA	2703		
Db	1034	ATCAATGTCAAGTACCAAAATGTTAATGTTGTTCAATTTAACTCTCCCTGAGACTTCA	1093		
QY	2704	GTGCACGTATATAGAGTCTAAACACACCTTAAGAGAAAAGATCAAAATTTTTCAGATG	2763		
Db	1094	GTGCACGTATATAGAGTCTAAACACACCTTAAGAGAAAAGATCAAAATTTTTCAGATG	1153		
QY	2764	ATTTCGAAATTTTCAATTCAGGTATTTGTAATAGTACATATATATATATATATATACAT	2823		
Db	1154	ATTTCGAAATTTTCAATTCAGGTATTTGTAATAGTACATATATATATATATATATACAT	1213		
QY	2824	CTCCTATCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGTATCATTC	2883		
Db	1214	CTCCTATCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGTATCATTC	1273		
QY	2884	CCTTTTCCATATAGGAAACATATTTTGAAGTGGCCAGATGAGTTTATCATGTCAAGTAA	2943		
Db	1274	CCTTTTCCATATAGGAAACATATTTTGAAGTGGCCAGATGAGTTTATCATGTCAAGTAA	1333		
QY	2944	AAATTAATACCCCAAAATGCCACCACTTAACGATTTTCACTCTCTTGGGTTTTCAT	3003		
Db	1334	AAATTAATACCCCAAAATGCCACCACTTAACGATTTTCACTCTCTTGGGTTTTCAT	1393		
QY	3004	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTTGTCACTTTTCAAGGGC	3063		
Db	1394	GTATGAACCTAACTCCCCACCCCAACATCTCCCTCCACATTTGTCACTTTTCAAGGGC	1453		
QY	3064	CCACAGTACTTTTGTGGGCAATTTTCCAGATGTTTACAGACTGTGAGTACAGCAAAA	3123		
Db	1454	CCACAGTACTTTTGTGGGCAATTTTCCAGATGTTTACAGACTGTGAGTACAGCAAAA	1513		
QY	3124	ATCTTTTACTAGTGTGTGTGTATATATATAAACAATTTGTAATTTCTTTAGCCCAT	3183		
Db	1514	ATCTTTTACTAGTGTGTGTGTATATATAAACAATTTGTAATTTCTTTAGCCCAT	1573		
QY	3184	TTTCTAGACTGTCTGTGGAAATATATTTGTGTGTGTATATATATATATATATATATAT	3243		
Db	1574	TTTCTAGACTGTCTGTGGAAATATATTTGTGTGTGTATATATATATATATATATATAT	1633		
QY	3244	ATGATAGGATTTAATCTAATCTAATTTGTCGCCGAGTTGTGCCAAGTGCATAGTC	3303		
Db	1634	ATGATAGGATTTAATCTAATCTAATTTGTCGCCGAGTTGTGCCAAGTGCATAGTC	1693		
QY	3304	TGAGCTAAATCTAGGTGATTTTCATCATGACAACTCCCTCCCTGAGTCCATTTAACCTGT	3363		
Db	1694	TGAGCTAAATCTAGGTGATTTTCATCATGACAACTCCCTCCCTGAGTCCATTTAACCTGT	1753		
QY	3364	AGCAACCTTCTGCATATATAAATCTTGAATCATGTACCATTACAAATGGGATATAAGA	3423		
Db	1754	AGCAACCTTCTGCATATATAAATCTTGAATCATGTACCATTACAAATGGGATATAAGA	1813		
QY	3424	GGCAGCGTAAAGCAGATGAGCTGTGGACTAGCAATATAGGCTTTTGTGGTGGTGG	3483		
Db	1814	GGCAGCGTAAAGCAGATGAGCTGTGGACTAGCAATATAGGCTTTTGTGGTGGTGG	1873		
QY	3484	TTTGATAAAGCAGATTTTGGGTCATATTTCTGCTGGAGCAAAAGTCAATACAC	3543		
Db	1874	TTTGATAAAGCAGATTTTGGGTCATATTTCTGCTGGAGCAAAAGTCAATACAC	1933		
QY	3544	TTTGAAGTATTTATTTCTTATCCCTCAATTCATGTTGGTGTGATGAAATGGCAGTTGT	3603		

Db 1934 TTTGAGTATTATATTGTTCTTATCTCAATTCAGTGGTGATGAATGCCAGGTGT 1993
 Qy 3604 CTGATATTTCTTTTCAGACTCCGCCAGACAGATGCTGATAATAATAGGTAAGATAATT 3663
 Db 1994 CTGATATTTCTTTTCAGACTCCGCCAGACAGATGCTGATAATAATAGGTAAGATAATT 2053
 Qy 3664 TGTGGGCCATATTTTAGGACAGGTAAATTAACATCAGTTCAGTTCGTTGAATTGCAA 3723
 Db 2054 TGTGGGCCATATTTTAGGACAGGTAAATTAACATCAGTTCAGTTCGTTGAATTGCAA 2113
 Qy 3724 GCCTAAGAAGTACTGCCCTTTTGTGTGTAGCAGTCAATCTATTATTCCACTGGCGCAT 3783
 Db 2114 GCCTAAGAAGTACTGCCCTTTTGTGTGTAGCAGTCAATCTATTATTCCACTGGCGCAT 2173
 Qy 3784 CATATGCAAGTATATGCTTATATATATAGCCATATAGTTCACACCATTTTGTAGACA 3843
 Db 2174 CATATGCAAGTATATGCTTATATATATAGCCATATAGTTCACACCATTTTGTAGACA 2233
 Qy 3844 ATTGCTTTTTTTTCAAGATGCTTTGTTCTTTTCATATGAAAAAATGCAATTTATAAAT 3903
 Db 2234 ATTGCTTTTTTTTCAAGATGCTTTGTTCTTTTCATATGAAAAAATGCAATTTATAAAT 2293
 Qy 3904 CAGAAAGTCATAGATTTCTGAAGCGCTCAACGTGCATTTTATTTATGACGTGGTAAGTAA 3963
 Db 2294 CAGAAAGTCATAGATTTCTGAAGCGCTCAACGTGCATTTTATTTATGACGTGGTAAGTAA 2353
 Qy 3964 CTGTGGTTTACTAGCAGGAATATTTCCAAATTTACCTTTACTACATCTTTTCAACAAGT 4023
 Db 2354 CTGTGGTTTACTAGCAGGAATATTTCCAAATTTACCTTTACTACATCTTTTCAACAAGT 2413
 Qy 4024 AACTTTGTAGAAATGAGCCAGCAAGCCAGGCGCTGAGTTGGCAGTGGCCCATATAAGTAA 4083
 Db 2414 AACTTTGTAGAAATGAGCCAGCAAGCCAGGCGCTGAGTTGGCAGTGGCCCATATAAGTAA 2473
 Qy 4084 AATAAAAGTTTACAGAAACCTT 4105
 Db 2474 AATAAAAGTTTACAGAAACCTT 2495

RESULT 4
 ABK94408
 ID ABK94408 standard; DNA: 2595 BP.
 XX AC ABK94408;
 XX DT 27-AUG-2002 (first entry)
 XX DE DNA encoding endothelin receptor A (EDNRA), exon 8.
 XX ...
 ...
 KW Endothelin; EDN; endothelin converting enzyme; ECE; EDNRA;
 KW endothelin receptor A; signaling system; cardiovascular disease;
 KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;
 KW fatty acid metabolism; diabetes; familial hypercholesterolemia;
 KW forensic marker; transgenic animal; solid support; SNP;
 KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT variation replace(1830,G)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX W0200224747-A2.
 XX PN 28-MAR-2002.
 XX PD 31-AUG-2001; 2001W0-EPI0087.
 XX PF 19-SEP-2000; 2000EP-0120123.
 XX PR (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX PA
 XX XX

PI Brinkmann U, Hoffmeyer S;
 XX WPI: 2002-435060/46.
 XX Novel polynucleotide of the endothelin/endothelin converting
 PT enzyme/receptors of endothelin and endothelin converting enzyme
 PT signaling system associated with cardiovascular disease, useful for
 PT treating the disease -
 XX
 PS Claim 1: Page -: 190pp; English.
 XX
 CC The invention describes a polynucleotide (I) of the endothelin
 CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
 CC signaling system which is associated with a cardiovascular disease. (I),
 CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
 CC or (II) is useful for producing cells capable of expressing a molecular
 CC variant polypeptide which is associated with a cardiovascular disease.
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
 CC a molecular variant gene comprising (I) is useful for identifying and
 CC obtaining a pro-drug or drug capable of modulating the activity of a
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
 CC or its gene product, or for identifying and obtaining an inhibitor of
 CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
 CC signaling system or its gene product. The isolated proteins and
 CC polynucleotides encoding them are useful for preparation of a
 CC pharmaceutical composition for treating a cardiovascular disease such as
 CC coronary heart disease, hypertension, atherosclerosis, or related to
 CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
 CC hypercholesterolemia. The gene or a polynucleotide fragment of the
 CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
 CC creating a transgenic animal and in creation of a solid support
 CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
 CC host cells of the invention. This sequence encodes the cardiovascular
 CC regulator Endothelin receptor A (EDNRA).
 CC Note: This sequence does not appear in the specification but has been
 CC obtained from GenBank using information given in the invention.
 XX SQ Sequence 2595 BP; 788 A; 478 C; 459 G; 870 T; 0 other;

Query Match 60.2%; Score 2470; DB 24; Length 2595;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1624 CCAGTCATGCCCTCTGCTGCTGTGTACCCAGTCCAAAAGCTGATGACCTCGGTCCCAT 1683
 Db 15 CCAGTCATGCCCTCTGCTGCTGTGTACCCAGTCCAAAAGCTGATGACCTCGGTCCCAT 74
 Qy 1684 GAACGGAAACAGCATCCAGTGGAAAGAACCCAGATCAAAACACACACACACGGAG 1743
 Db 75 GAACGGAAACAGCATCCAGTGGAAAGAACCCAGATCAAAACACACACACACGGAG 134
 Qy 1744 CAGCCATAGGACACATGAACCTGACCCCTTAGAAGCAGCTCTCGGTACTCCCATAT 1803
 Db 135 CAGCCATAGGACACATGAACCTGACCCCTTAGAAGCAGCTCTCGGTACTCCCATAT 194
 Qy 1804 CCTCTCGGAGAAAAAATCACAAGCAACTGTGACTCCGGGAATCTCTCTGATCCTT 1863
 Db 195 CCTCTCGGAGAAAAAATCACAAGCAACTGTGACTCCGGGAATCTCTCTGATCCTT 254
 Qy 1864 CTTCTTAAATTCACCTCCACACCCCAAGAAAGTGTTCCTTCCAAACCCGGAAGTAGCTG 1923
 Db 255 CTTCTTAAATTCACCTCCACACCCCAAGAAAGTGTTCCTTCCAAACCCGGAAGTAGCTG 314
 Qy 1924 GTTTATCCACCCACACATCTACGATCGTACTCTTTTAAATTCATCTAATTTACATATTC 1983
 Db 315 GTTTATCCACCCACACATCTACGATCGTACTCTTTTAAATTCATCTAATTTACATATTC 374
 Qy 1984 TCGGTGTTGTTATTCAGCACTAAATAATGTGGAGCTGGGGAGAAATGAAGACTGTAA 2043
 Db 375 TCGGTGTTGTTATTCAGCACTAAATAATGTGGAGCTGGGGAGAAATGAAGACTGTAA 434
 Qy 2044 TGAACCCAGAGATATTTTACTACTTTTTCATGAAATAGAGCTTTCAAGTACATGGCTA 2103

Db	435	TCGAACCAAGGATATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATACGCTA	494
Qy	2104	GCCTTTATGGCAGTCTCGTGAATGTTCAATGGGAACGTGTCACCACTGAACACTTTAGAGA	2163
Db	495	GCCTTTATGGCAGTCTCGTGAATGTTCAATGGGAACGTGTCACCACTGAACACTTTAGAGA	554
Qy	2164	TTAAGCACAGAATTTCTACTTTTTTTTAAAGTGATTTTTTGTCTTCAGGCAAAACACAATA	2223
Db	555	TTAAGCACAGAATTTCTACTTTTTTTTAAAGTGATTTTTTGTCTTCAGGCAAAACACAATA	614
Qy	2224	TGGGCTCAGGTACATTTTATTTGAAATGTCATTTTGGTGGCAGTATTTTTTAACTGCATTA	2283
Db	615	TGGGCTCAGGTACATTTTATTTGAAATGTCATTTTGGTGGCAGTATTTTTTAACTGCATTA	674
Qy	2284	TAGCCTAACATCATTTATTTGAACCTTATTTACACATAGTTTGAAGAAAAAAGACAAAAAT	2343
Db	675	TAGCCTAACATCATTTATTTGAACCTTATTTACACATAGTTTGAAGAAAAAAGACAAAAAT	734
Y	2344	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACACTATTTATTTTTTAAAAACA	2403
Db	735	AGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACACTATTTATTTTTTAAAAACA	794
Qy	2404	CAAAATTCCTAAAGCTACACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	2463
Db	795	CAAAATTCCTAAAGCTACACAAATACTACAGGCCCTTAAAGCACAGTCTGATGACACATTT	854
Qy	2464	GGCAGTTTAAATAGATGTTACTCAAGAAATTTTTTAAAGAACTGTATTTTATTTTTTAAATG	2523
Db	855	GGCAGTTTAAATAGATGTTACTCAAGAAATTTTTTAAAGAACTGTATTTTATTTTTTAAATG	914
Qy	2524	GTGTTTTTATACAGGGACCTTTGAACATGCTTTGTATGTATTTAAATTCAAAAGTAATGCTTC	2583
Db	915	GTGTTTTTATACAGGGACCTTTGAACATGCTTTGTATGTATTTAAATTCAAAAGTAATGCTTC	974
Qy	2584	AATCAGATAGTTCTTTTTTCCAAAGTTCAAATCTGTTTTTCACTGTAATTTTGTATGAAAA	2643
Db	975	AATCAGATAGTTCTTTTTTCCAAAGTTCAAAT - CTGTGTTTTTCACTGTAATTTTGTATGAAAA	1033
Qy	2644	ATCAATGTCAAGTACCAAAATCTTAATGATGTGTGCATTTAACTCTGCCTGAGACATTTCA	2703
Db	1034	ATCAATGTCAAGTACCAAAATCTTAATGATGTGTGCATTTAACTCTGCCTGAGACATTTCA	1093
Qy	2704	GTGCACCTGTATAGAAGTCTAAAAACACACACCTTAAGAGAAAAAGATCGAATTTTTCAGATG	2763
Db	1094	GTGCACCTGTATAGAAGTCTAAAAACACACACCTTAAGAGAAAAAGATCGAATTTTTCAGATG	1153
Y	2764	ATTCGGAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	2823
Db	1154	ATTCGGAATTTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATATACATATCAC	1213
Qy	2824	CTCCCTATCTCTAAATTTTGTGTTAAATCTGTTAACTGGCAGTAAGTCTTTTTCATCATCTC	2883
Db	1214	CTCCCTATCTCTAAATTTTGTGTTAAATCTGTTAACTGGCAGTAAGTCTTTTTCATCATCTC	1273
Qy	2884	COTTTTCCATATAGGAACATAAATTTTGAAGTGGCCAGATGAGTATTTATCATGTGCAAGTAA	2943
Db	1274	COTTTTCCATATAGGAACATAAATTTTGAAGTGGCCAGATGAGTATTTATCATGTGCAAGTAA	1333
Qy	2944	AAATAAATTTACCCACAAAATGCCACACAGTAACCTTAACGATTCCTTCACATCTTTGGGGTTTCA	3003
Db	1334	AAATAAATTTACCCACAAAATGCCACACAGTAACCTTAACGATTCCTTCACATCTTTGGGGTTTCA	1393
Qy	3004	GTATCAACCTTAACCTCCACACCAACATCTCCCTCCACATGTCACCAATTTCAAAAGGGC	3063
Db	1394	GTATGAACCTTAACCTCCACACCAACATCTCCCTCCACATGTCACCAATTTCAAAAGGGC	1453
Qy	3064	CCACAGTGACATTTTGGTGGGCATTTTCCACAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGACATTTTGGTGGGCATTTTCCACAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTACGCCATTT	3183
Db	1514	ATCTTTTACTAGTGTGTGTATATATATAAACAATTTGTAATTTCTTTTACGCCATTT	1573

RESULT 5
ABK35492
ID ABK35492 standard; DNA; 2595 BP.
XX
AC ABK35492;
XX
08-MAY-2002 (first entry)

Db	1394	GTATGAACCTAACTCCCAACCCCAACATCTCCCTCCACATTCGTCCACATTTCTCAAGGGC	1453
Qy	3064	CCACAGTGTACTTTTGGTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	3123
Db	1454	CCACAGTGTACTTTTGGTGGGCATTTTCCAGATGTTTACAGACTGTGAGTACAGCAGAAA	1513
Qy	3124	ATCTTTTACTAGTGTGTGTGTATATATAAACAATTTGTAATTTCTTTTAGCCCATTT	3183
Db	1514	ATCTTTTACTAGTGTGTGTATATATAAACAATTTGTAATTTCTTTTAGCCCATTT	1573
Qy	3184	TTTCTAGACTGTCTGTGGGAATATATTTGTGTGTGATATATGATGTGTGTGATGGT	3243
Db	1574	TTTCTAGACTGTCTGTGGGAATATATTTGTGTGTGATATATGATGTGTGTGATGGT	1633
Qy	3244	ATGTATGGATTTAACTTAATTAATTTGCCCGCAGTTGTGCCAAAGTGCATAGTC	3303
Db	1634	ATGTATGGATTTAACTTAATTAATTTGCCCGCAGTTGTGCCAAAGTGCATAGTC	1693
Qy	3304	TTAGCTAAATCTAGGTGATTTTCATCATGACAACTGCCTCAGTCCATTTTAACTGT	3363
Db	1694	TTAGCTAAATCTAGGTGATTTTCATCATGACAACTGCCTCAGTCCATTTTAACTGT	1753
Qy	3364	AGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTACCATTACAAATGGGATATAAGA	3423
Db	1754	AGCAACCTTCTGCATTCATAAATCTTGTAAATCATGTACCATTACAAATGGGATATAAGA	1813
Qy	3424	GGCAGCTGAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTGGTTGGTTGG	3483
Db	1814	GGCAGCTGAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTTGTGGTTGGTTGG	1873
Qy	3484	TTTGATAAGCAGTATTTGGGGTGCATATTTGTTCTGTCTGGAGCAAAAGTCATTACAC	3543
Db	1874	TTTGATAAGCAGTATTTGGGGTGCATATTTGTTCTGTCTGGAGCAAAAGTCATTACAC	1933
Qy	3544	TTTGAAGTATTATTTGTTCTTATCCTCAATTCATGTGGTGTGATGAAATTTGCCAGTTGT	3603
Db	1934	TTTGAAGTATTATTTGTTCTTATCCTCAATTCATGTGGTGTGATGAAATTTGCCAGTTGT	1993
Qy	3604	CTGATATTTCTTCAGACTTCGCCAGACAGATTCGTGATAATAAATTAGTAAAGATAAT	3663
Db	1994	CTGATATTTCTTCAGACTTCGCCAGACAGATTCGTGATAATAAATTAGTAAAGATAAT	2053
Qy	3664	TGTTGGGCCATTTTATAGCAGAGTAAATAACATCAGGTTCCAGTTGCTTGAATTTGCCAA	3723
Db	2054	TGTTGGGCCATTTTATAGCAGAGTAAATAACATCAGGTTCCAGTTGCTTGAATTTGCCAA	2113
Qy	3724	GGCTAAGAAGTACTGCCCCCTTTTGTGTGTAGCAGTCAAATCTATTATTCACCTGGCGCAT	3783
Db	2114	GGCTAAGAAGTACTGCCCCCTTTTGTGTGTAGCAGTCAAATCTATTATTCACCTGGCGCAT	2173
Qy	3784	CATATGCACTGATATATGCCCTATAATAAGCCATAGGTTACACACATTTTGTGTTAGACA	3843
Db	2174	CATATGCACTGATATATGCCCTATAATAAGCCATAGGTTACACACATTTTGTGTTAGACA	2233
Qy	3844	ATTGCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCAATTTTATAAAT	3903
Db	2234	ATTGCTTTTTTTTCAAGATGCTTTGTTTCTTTCATATGAAAAAATGCAATTTTATAAAT	2293
Qy	3904	CAGAAAGTCATAGATTTCTGAAGGGGTCAACGTGCAATTTTATTTATGGAAGTAA	3963
Db	2294	CAGAAAGTCATAGATTTCTGAAGGGGTCAACGTGCAATTTTATTTATGGAAGTAA	2353
Qy	3964	CTGTGGTTTACTACAGCAATATTTCCCAATTTCTACCTTTTACTACATCTTTTCAACAAGT	4023
Db	2354	CTGTGGTTTACTACAGCAATATTTCCCAATTTCTACCTTTTACTACATCTTTTCAACAAGT	2413
Qy	4024	AACCTTTGTAGAAATGAGCCAGAACCAAGGCCCTGAGTTGGCAGTGGCCCAAGTGTAA	4083
Db	2414	AACCTTTGTAGAAATGAGCCAGAACCAAGGCCCTGAGTTGGCAGTGGCCCAAGTGTAA	2473
Qy	4084	AATAAAAGTTTACAGAAACCTT 4105	

Db 2474 AATRAAGCTTTACAGAAACCTT 2495

RESULT 6
AAF20903
ID AAF20903 standard; DNA; 1868 BP.
XX AC
XX AAF20903;
XX DT 14-MAR-2001 (first entry)
XX
XX DE Human low adenosine antisense oligonucleotide #2470.
XX
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX OS
XX Homo sapiens.
XX
XX WO2000062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US08020.
XX
XX 06-APR-1999; 99US-0127958.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX
XX Nyce JW;
XX
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
XX
XX Disclosure; Page 676; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
XX oligonucleotides and compositions (I) comprising them. In the antisense
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX the antisense oligonucleotides and (I) can be used to down-regulate the
XX expression and or activity of target polypeptides associated with
XX lung/respiratory disorders and malignancies, such as stimulating and
XX activating peptide factors and transmitters, transcription factors,
XX immunoglobulins and antibodies, antibody receptors, cytokines and
XX chemokines, endogenously produced specific and non-specific enzymes,
XX binding proteins, adhesion molecules and their receptors, cytokine and
XX chemokine receptors, adenosine receptors, bradykinin receptors, central
XX nervous system (CNS) and peripheral nervous and non-nervous system
XX receptors, CNS and peripheral nervous and non-nervous system peptide
XX transmitters, defensins, growth factors, vasoactive peptides and
XX receptors, binding proteins and malignancy associated proteins. The
XX antisense oligonucleotides may be used in this way to treat disorders
XX including respiratory obstruction (especially pulmonary obstruction
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
XX and/or surfactant hypoproduction which are associated with a disease or
XX condition selected from pulmonary vasoconstriction, inflammation,
XX allergies, asthma, impeded respiration, respiratory distress syndrome
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX

CC and/or cancer, AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 other;

Query Match	44.3%	Score 1819.6	DB 21	Length 1868
Best Local Similarity	99.7%	Pred. No. 0		
Matches 1844	Conservative 0	Mismatches 4	Indels 2	Gaps 2
QY 421	AAAAAGTGAAGCTGTAAAAGCAGCACAAGTGC	AAATGAAGAGATATTCTCTCAAAATTTGGCT	480	
DB	10	AAAAAGTGAAGCTGTAAAAGCAGCACAAGTGC	AAATGAAGAGATATTCTCTCAAAATTTGGCT	69
QY 481	CAAGATGGAACCCCTTTGGCCTCAGGGCATCCT	TTTGGCTGGCAGCTGGTGGAGTGTAAAT	540	
DB	70	CAAGATGGAACCCCTTTGGCCTCAGGGCATCCT	TTTGGCTGGCAGCTGGTGGAGTGTAAAT	129
QY 541	CAGTGATAATCCTCAGAGATACACACAAAATCT	TAGCAATCATGCGGATGATTTCACAC	600	
DB	130	CAGTGATAATCCTCAGAGATACACACAAAATCT	TAGCAATCATGCGGATGATTTCACAC	189
QY 601	TTTTCTGGGCACAGAGCTCAGCTTCCTGGTTAC	CACCTCATCAACCCACTAAATTTGGTGCT	660	
DB	190	TTTTCTGGGCACAGAGCTCAGCTTCCTGGTTAC	CACCTCATCAACCCACTAAATTTGGTGCT	249
QY 661	ACCAGCAATGGCTCAATGCACAACTATGCCCC	ACAGACAGACTAAAAATTACTTCAGCTTT	720	
DB	250	ACCAGCAATGGCTCAATGCACAACTATGCCCC	ACAGACAGACTAAAAATTACTTCAGCTTT	309
QY 721	CAATACATTAACACTGTGATATCTTGTTACTAT	TTTTTCATCTGGGAATGGTGGGAATGC	780	
DB	310	CAATACATTAACACTGTGATATCTTGTTACTAT	TTTTTCATCTGGGAATGGTGGGAATGC	369
QY 781	AACTCTGCTCAGGATCATTTACAGACAATATGT	ATGAGGAATGCCCCACAGCGCTCAT	840	
DB	370	AACTCTGCTCAGGATCATTTACAGACAATATGT	ATGAGGAATGCCCCACAGCGCTCAT	429
QY 841	AGCGAGTCTTCCCTTGGAGACCTTATCTATGT	GGTCAATGATCCTCATCAATGTATTT	900	
DB	430	AGCGAGTCTTCCCTTGGAGACCTTATCTATGT	GGTCAATGATCCTCATCAATGTATTT	489
QY 901	TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGAT	CAACAATGACTTTGGCGTATTTCTTTGCAA	960	
DB	490	TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGAT	CAACAATGACTTTGGCGTATTTCTTTGCAA	549
QY 961	CTGTGTTCCCTTTTTCAGAAAGTCCCTCGTGG	GGATCACCGTCTCAACCTCTCGCTCT	1020	
DB	550	CTGTGTTCCCTTTTTCAGAAAGTCCCTCGTGG	GGATCACCGTCTCAACCTCTCGCTCT	609
QY 1021	TAGTGTTGACAGGTACAGACAGTTGGCTCCT	CGAGTCGTTCAGGGAATTTGGGATTC	1080	
DB	610	TAGTGTTGACAGGTACAGACAGTTGGCTCCT	CGAGTCGTTCAGGGAATTTGGGATTC	669
QY 1081	TTTGGTAACTGCCATTGCAATTTGTCCTCAT	CTGGATCCTGTCTTATCTCGGCAATTC	1140	
DB	670	TTTGGTAACTGCCATTGCAATTTGTCCTCAT	CTGGATCCTGTCTTATCTCGGCAATTC	729
QY 1141	TGAAGCGATTGGCTTCTGTCATGGTACCCCT	TTTGAATATAGGGGTGAACAGCATAAACTG	1200	
DB	730	TGAAGCGATTGGCTTCTGTCATGGTACCCCT	TTTGAATATAGGGGTGAACAGCATAAACTG	789
QY 1201	TATGCTCAATGCCACATCAAAATTCATGGAG	TTCTACCAAGATCTAAAGGACTGGTGCT	1260	
DB	790	TATGCTCAATGCCACATCAAAATTCATGGAG	TTCTACCAAGATCTAAAGGACTGGTGCT	849
QY 1261	CTTTCGGGTTCTATTTCCTGTATGCCCTTGG	TGTGCACATCTCTACACCCCTCATGAC	1320	
DB	850	CTTTCGGGTTCTATTTCCTGTATGCCCTTGG	TGTGCACATCTCTACACCCCTCATGAC	909
QY 1321	TTGTGAGATGTTGAACAGAAGGAATGGCAGTT	GGAGAAATTTGCCCTCAGTGAACATCTTAA	1380	
DB	910	TTGTGAGATGTTGAACAGAAGGAATGGCAGTT	GGAGAAATTTGCCCTCAGTGAACATCTTAA	969

KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX WO2000062736-A2.
 PN 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US08020.
 PF 06-APR-1999; 99US-0127958.
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure; Page 244; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 other;

Query Match 44.3%; Score 1819.6; DB 21; Length 1868;
 Best Local Similarity 99.7%; Pred No. 0;
 Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 421 AAAAAGTGAAGGTGTAAGACGACCAAGTGCATAAGAGATATTTCCCAAAATTTGCCT 480
 DB 10 AAAAAGTGAAGGTGTAAGACGACCAAGTGCATAAGAGATATTTCCCAAAATTTGCCT 69

QY 481 CAAGATGGAACCCCTTTGGCTCAGGGCATCCTTTTGGCTGGCACTGGTGGATGTGAAT 540
 DB 70 CAAGATGGAACCCCTTTGGCTCAGGGCATCCTTTTGGCTGGCACTGGTGGATGTGAAT 129
 QY 541 CAGTGAATATCTTGAGAGATACAGCAAAATCTAAGCAATCATGTGGATGATTTACACAC 600
 DB 130 CAGTGAATATCTTGAGAGATACAGCAAAATCTAAGCAATCATGTGGATGATTTACACAC 189
 QY 601 TTTTCTGGCACAGACTCAGCTTCCCTGGTTACCACTCATCAACCCACTAATTTGGTCCCT 660
 DB 190 TTTTCTGGCACAGACTCAGCTTCCCTGGTTACCACTCATCAACCCACTAATTTGGTCCCT 249
 QY 661 ACCAGCAATGGCTCAATGACCAACTATTGCCACACAGACTAAAAATTTACTTCAGCTTT 720
 DB 250 ACCAGCAATGGCTCAATGACCAACTATTGCCACACAGACTAAAAATTTACTTCAGCTTT 309
 QY 721 CAAATACATTAAACACTGTGATATCTTGATCTATTTTTCATCGTGGGAATGTTGGGAATGC 780
 DB 310 CAAATACATTAAACACTGTGATATCTTGATCTATTTTTCATCGTGGGAATGTTGGGAATGC 369
 QY 781 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGCCCCACGCGCTGAT 840
 DB 370 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGCCCCACGCGCTGAT 429
 QY 841 AGCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCAATGATCTCCCTATCAATGTATT 900
 DB 430 AGCAGTCTTGCCCTTGGAGACCTTATCTATGTGGTCAATGATCTCCCTATCAATGTATT 489
 QY 901 TAAGCTGCTGGCTGGGCGCTGGGCTTTTGTATCAACAATGACTTTTGGCGTATTTCTTTCGAA 960
 DB 490 TAAGCTGCTGGCTGGGCGCTGGGCTTTTGTATCAACAATGACTTTTGGCGTATTTCTTTCGAA 549
 QY 961 GCTGTTCCCTTTTGGAGAACTCTCGGTGGGATCACGCTCCTCAACCTCTCGGCTCT 1020
 DB 550 GCTGTTCCCTTTTGGAGAACTCTCGGTGGGATCACGCTCCTCAACCTCTCGGCTCT 609
 QY 1021 TACTGTTGACAGGTACAGACAGCTGCTCTCTGGAGTCTGTTTTCAGGGAATTTGGGATTC 1080
 DB 610 TACTGTTGACAGGTACAGACAGCTGCTCTCTGGAGTCTGTTTTCAGGGAATTTGGGATTC 669
 QY 1081 TTTGGTAATGCCATGAAATGTCCTCATCTGGATCCTGTCCTTTATPCTGGGCAATTC 1140
 DB 670 TTTGGTAATGCCATGAAATGTCCTCATCTGGATCCTGTCCTTTATPCTGGGCAATTC 729
 QY 1141 TGAAGCGATGGCTGCTCATGTGTACCTTTGAATATAGGGGTGAACAGCATAAACCTG 1200
 DB 730 TGAAGCGATGGCTGCTCATGTGTACCTTTGAATATAGGGGTGAACAGCATAAACCTG 789
 QY 1201 TATGCTCAATGCCACATCAAAATTCATGGAGTCTTACCAAGATGTAAGGACTGGTGCT 1260
 DB 790 TATGCTCAATGCCACATCAAAATTCATGGAGTCTTACCAAGATGTAAGGACTGGTGCT 849
 QY 1261 CTTCCGGTCTTATTTCTGTATGCCCTTGGTGGCACTGCGATCTTACACCCCTCATGAC 1320
 DB 850 CTTCCGGTCTTATTTCTGTATGCCCTTGGTGGCACTGCGATCTTACACCCCTCATGAC 909
 QY 1321 TTGTGAGATGTTGAACAGAGGAATGCGACCTTGAGAAATTTGCCCTCAGTGAACATCTTAA 1380
 DB 910 TTGTGAGATGTTGAACAGAGGAATGCGACCTTGAGAAATTTGCCCTCAGTGAACATCTTAA 969
 QY 1381 GCAGGCTGAGAGAGTGGCAAAACAGTTTCTGCTGTTGTAATTTTGGTCTTTGGCTG 1440
 DB 970 GCAGGCTGAGAGAGTGGCAAAACAGTTTCTGCTGTTGTAATTTTGGTCTTTGGCTG 1029
 QY 1441 GTTCCCTCTTCACTTAAGCGGTATATTGAAGAAACCTGTGTATTAACGAAATGGACAAGAA 1500
 DB 1030 GTTCCCTCTTCACTTAAGCGGTATATTGAAGAAACCTGTGTATTAACGAGATGGACAAGAA 1089
 QY 1501 CCGATGTGAATTAATTTCTTACTGCTCATCGGATTAATCATCGGATTAATTTGCGCAAC 1560
 DB 1090 CCGATGTGAATTAATTTCTTACTGCTCATCGGATTAATCATCGGATTAATTTGCGCAAC 1149
 QY 1561 CATGAATTCATGTATAAACCCCATGCTCTGTATTGTTGTGAGCAAGAAATTTAAAAATTTG 1620

Db 1150 CATGAATTCATGTATAAACCCTCATAGCTCTGATTTTGTGACGAAGAAATTTAAAAATTG 1209
 QY 1621 TTTCCAGTCATGCTCTGCTGCTGTGTACAGTCCAAAGTCTGATGACCTCGGTCCC 1680
 Db 1210 TTTCCAGTCATGCTCTGCTGCTGTGTACAGTCCAAAGTCTGATGACCTCGGTCCC 1269
 QY 1681 CATGAACGGAAACAGCATCCAGTGGAGAACCAACGATCAAAACACCAACACAGACCG 1740
 Db 1270 CATGAACGGAAACAGCATCCAGTGGAGAACCAACGATCAAAACACCAACACAGACCG 1329
 QY 1741 GAGCAGCATAAGACAGCATGAACTGACCAACCTTGAAGCACTCTCTCGTATCCCAT 1800
 Db 1330 GAGCAGCATAAGACAGCATGAACTGACCAACCTTGAAGCACTCTCTCGTATCCCAT 1389
 QY 1801 AATCCTCTCGGAGAAATAATCAAGCACTGCTGCTCGGGAATCTTCTCTGATC 1860
 Db 1390 AATCCTCTCGGAGAAATAATCAAGCACTGCTGCTCGGGAATCTTCTCTGATC 1449
 QY 1861 CTCTCTCTTAATTCACCTCCACACCAACCAAGAAATGCTTTCCAAACCGCAA-GGTAG 1919
 Db 1450 CTCTCTCTTAATTCACCTCCACACCAACCAAGAAATGCTTTCCAAACCGCAAGGGTAG 1509
 QY 1920 ACTGGTTTATCCACCCACACATCTAGCAATCGTCTCTTTAATGATCTAATTTACAT 1979
 Db 1510 ACTGGTTTATCCACCCACACATCTAGCAATCGTCTCTTTAATGATCTAATTTACAT 1569
 QY 1980 ATCTCTGCTGTGATTCAGCACTTAAATGCTGGAGCTGGGAGATGAAGACTGT 2039
 Db 1570 ATCTCTGCTGTGATTCAGCACTTAAATGCTGGAGCTGGGAGATGAAGACTGT 1629
 QY 2040 TAAATGAACACGAGGATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG 2099
 Db 1630 TAAATGAACACGAGGATTTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG 1689
 QY 2100 GCTAGCTTTATGCGAGTCTGCTGGAATGTTCAAGTGAAGTGTGCTACCAATGAACTTTA 2159
 Db 1690 GCTAGCTTTATGCGAGTCTGCTGGAATGTTCAAGTGAAGTGTGCTACCAATGAACTTTA 1749
 QY 2160 GAGATTAACGACAGATTTCTACTTTTAACTGTA-TTTTGTCTCTCAGGCCAACA 2218
 Db 1750 GAGATTAACGACAGATTTCTACTTTTAACTGTA-TTTTGTCTCTCAGGCCAACA 1809
 QY 2219 CAATATGGCTCAGGTCACATTTTATTTGAATGTCATTTGGTGCCAGTAT 2268
 Db 1810 CAATATGGCTCAGGTCACATTTTATTTGAATGTCATTTGGTGCCAGTAT 1859
 RESULT 8
 -A34781
 AAA34781 standard; DNA; 1868 BP.
 AC AAA34781;
 XX
 DT 28-JUL-2000 (first entry)
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2470.
 DE
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytoskeletal; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX

03-AUG-1999; 99WO-US17712.
 03-AUG-1998; 98US-0095212.
 (UYEC-) UNIV EAST CAROLINA.
 Nyce JW;
 WPI; 2000-205971/18.
 New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers
 Disclosure; Page 606-607; 1343pp; English.
 The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA3313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.
 Sequence 1868 BP; 512 A; 419 C; 389 G; 548 T; 0 other;

Query Match 44.3%; Score 1819.6; DB 21; Length 1868;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 QY 421 AAAAAGTGAAGTGTAAAGCAGCAGCAAGTGCATTAAGAGATATTTCTCAAAATTTGCC 480
 Db 10 AAAAAGTGAAGTGTAAAGCAGCAGCAAGTGCATTAAGAGATATTTCTCAAAATTTGCC 69
 QY 481 CAAGATGGAAACCCCTTTGCCCTCAGGGCATCTTTTGGCTGGCAGCTGGTGGATGTAA 540
 Db 70 CAAGATGGAAACCCCTTTGCCCTCAGGGCATCTTTTGGCTGGCAGCTGGTGGATGTAA 129
 QY 541 CAGTGATTAATCCTGAGAGATCAGCACAATAATCTAAGCAATCATGTGGATGATTTCACAC 600
 Db 130 CAGTGATTAATCCTGAGAGATCAGCACAATAATCTAAGCAATCATGTGGATGATTTCACAC 189
 QY 601 TTTTCTGGGCACAGCTCAGCTTCTGTTACCACTCATCAACCCACTAATTTGGTCT 660
 Db 190 TTTTCTGGGCACAGCTCAGCTTCTGTTACCACTCATCAACCCACTAATTTGGTCT 249
 QY 661 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTTACTTCAGCTTT 720
 Db 250 ACCCAGCAATGGCTCAATGCACAACTATTGCCACAGCAGACTAAAATTTACTTCAGCTTT 309
 QY 721 CAATACATTAACACTGTGATATCTTGTACTATTTTTCATCTGTTGGGAATGGTGGGAATGC 780
 Db 310 CAATACATTAACACTGTGATATCTTGTACTATTTTTCATCTGTTGGGAATGGTGGGAATGC 369

QY 781 AACTCTGCTCAGGATCATTACCAACAATAATCTATAGGAATGGCCCAACGCCGCTGAT 840
Db AACTCTGCTCAGGATCATTACCAACAATAATCTATAGGAATGGCCCAACGCCGCTGAT 429
QY 841 AGCAGTCTTCCCTTGAGAGCTTATCTATGCTGCTATGATCTCCCTATCAATGTAT 900
Db AGCAGTCTTCCCTTGAGAGCTTATCTATGCTGCTATGATCTCCCTATCAATGTAT 489
QY 901 TAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db TAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
QY 961 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TAGTGTGACAGGTACAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db TAGTGTGACAGGTACAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 669
QY 1081 TTTGGTAACCTGCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db TTTGGTAACCTGCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
QY 1141 TGAAGCGATTGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db TGAAGCGATTGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789
QY 1201 TATGCTCAATGCCACATCAAAATTCATGAGTCTTACCAAGATGTAAAGGACTGGTGCT 1260
Db TATGCTCAATGCCACATCAAAATTCATGAGTCTTACCAAGATGTAAAGGACTGGTGCT 849
QY 1261 CTTCGGCTCTATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db CTTCGGCTCTATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
QY 1321 TTGTGAGATGTGAACAGAGGAAATGCGAGCTTGCAGATTCGCCCTCAGTGACATCTTAA 1380
Db TTGTGAGATGTGAACAGAGGAAATGCGAGCTTGCAGATTCGCCCTCAGTGACATCTTAA 969
QY 1381 GCAGCTGCGAGAGTGGCAAAACAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db GCAGCTGCGAGAGTGGCAAAACAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1029
QY 1441 GTTCCCTCTTCACTTAAGCGTATATGAAGAAACCTGTGTATACGAAATGGACAAGAA 1500
Db GTTCCCTCTTCACTTAAGCGTATATGAAGAAACCTGTGTATACGAGATGGACAAGAA 1089
QY 1501 CCGATGGAATTAATTAATTTCTTACTGCTCATGATTTACATCGTATTAATTTGGCAAC 1560
Db CCGATGGAATTAATTAATTTCTTACTGCTCATGATTTACATCGTATTAATTTGGCAAC 1149
QY 1561 CATGAATTCATGATTAACCCCATAGCTCTGATTTTGTGAGCAAGAAATTTAAATAATG 1620
Db CATGAATTCATGATTAACCCCATAGCTCTGATTTTGTGAGCAAGAAATTTAAATAATG 1209
QY 1621 TTTCCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db TTTCCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1269
QY 1681 CATGAACGGACAGCATCCAGTGGAGAACACACGATCAAAACCAACACACAGACCG 1740
Db CATGAACGGACAGCATCCAGTGGAGAACACACGATCAAAACCAACACACAGACCG 1329
QY 1741 GAGCAGCATAAGGACAGCATGAACTGACCACTTGAAGCACTCTCGGTACTCCCAT 1800
Db GAGCAGCATAAGGACAGCATGAACTGACCACTTGAAGCACTCTCGGTACTCCCAT 1389
QY 1801 AATCTCTCGGAGAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTCTCTGATC 1860
Db AATCTCTCGGAGAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTCTCTGATC 1449
QY 1861 CTTCTCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1919

Db 1450 CTTCTCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1509
QY 1920 ACTGGTTTATCACCACACACATCTACGAATCTACTCTCTTAAATGATCTAATTTACAT 1979
Db 1510 ACTGGTTTATCACCACACACATCTACGAATCTACTCTCTTAAATGATCTAATTTACAT 1569
QY 1980 ATTCTCGTGTGTATTTCAGCACTAAATAATGCTGGGAGCTGGGGAGAGTGAAGACTGT 2039
Db 1570 ATTCTCGTGTGTATTTCAGCACTAAATAATGCTGGGAGCTGGGGAGAGTGAAGACTGT 1629
QY 2040 TAAATGAAACACAGAGATATTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG 2099
Db 1630 TAAATGAAACACAGAGATATTACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG 1689
QY 2100 GCTAGCTTTTATGGCAGTTCTGCTGATGTTTCAATGGGAACTGGTCAACATGAACCTTTA 2159
Db 1690 GCTAGCTTTTATGGCAGTTCTGCTGATGTTTCAATGGGAACTGGTCAACATGAACCTTTA 1749
QY 2160 GAGATTACGACAAAGATTTTCTACTTTTAAAGTGA- TTTTGTGCTTTCAGCCAAACA 2218
Db 1750 GAGATTACGACAAAGATTTTCTACTTTTAAAGTGA- TTTTGTGCTTTCAGCCAAACA 1809
QY 2219 CAATATGGCTCAGGTCACCTTTTATTTGAAATCTCATTTTGGTCCAGTAT 2268
Db 1810 CAATATGGCTCAGGTCACCTTTTATTTGAAATCTCATTTTGGTCCAGTAT 1859

RESULT.9

AAA34793

ID AAA34793 standard; DNA; 1868 BP.

XX AAA34793;

AC AC

XX XX

DT 28-JUL-2000 (first entry)

XX XX

DE Human adenosine receptor related polynucleotide SEQ ID NO:2482.

XX XX

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphorothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiallergic; antiasthmatic; cytoskeletal; analgesic; impaired airway;

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO200009525-A2.

PN WO200009525-A2.

XX XX

PD 24-FEB-2000.

XX XX

XX 03-AUG-1999; 99WO-US17712.

XX XX

PR 03-AUG-1998; 98US-0095212.

XX XX

PA (UYEC-) UNIV EAST CAROLINA.

XX XX

PI Nyce JW;

XX XX

DR WPI; 2000-205971/18.

XX XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension,

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers

XX XX

PS Disclosure; Page 645-646; 1343pp; English.

XX XX

CC The present invention describes a new composition comprising an

CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which

CC targets nucleic acids involved in bronchoconstriction, allergies, and/or

Db 1750 GAGATTAACACAGATTTTCTACTTTTAAAGTGATTTTCTTCTCAGCCAAACA 1809
 QY 2219 CAATATGGGCTCAGTCACCTTTTATTTGAATGTCATTTGGTGCAGTAT 2268
 Db 1810 CAATATGGGCTCAGTCACCTTTTATTTGAATGTCATTTGGTGCAGTAT 1859

RESULT 10
 AAF20904
 ID AAF20904 standard; DNA; 2008 BP.
 XX AAF20904;
 XX AAF20904;
 DT 14-MAR-2001 (first entry)
 XX Human low adenosine antisense oligonucleotide #2471.

W Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 human; airway disorder; bronchoconstriction; lung inflammation;
 surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 respiratory obstruction; pulmonary obstruction; impeded respiration;
 surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 cancer; ss.

XX Homo sapiens.
 OS Wo2000062736-A2.
 XX 26-OCT-2000.
 XX 24-MAR-2000; 2000WO-US08020.
 PR 06-APR-1999; 99US-0127958.
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX Nyce JW:
 PI WPI; 2000-679539/66.
 XX Low adenosine (A) content antisense oligonucleotides which do not
 trigger adenosine receptors during metabolism, useful e.g. for treating
 cancers and respiratory obstructions -
 XX Disclosure; Page 676-677; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 oligonucleotides and compositions (I) comprising them. In the antisense
 oligonucleotides the A is replaced by a 'universal' or alternative base.
 (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 The antisense oligonucleotides and (I) can be used to down-regulate the
 expression and or activity of target polypeptides associated with the
 lung/respiratory disorders and malignancies, such as stimulating and
 activating peptide factors and transmitters, transcription factors,
 immunoglobulins and antibodies, antibody receptors, cytokines and
 chemokines, endogenously produced specific and non-specific enzymes,
 binding proteins, adhesion molecules and their receptors, cytokine and
 chemokine receptors, adenosine receptors, bradykinin receptors, central
 nervous system (CNS) and peripheral nervous and non-nervous system
 receptors, CNS and peripheral nervous and non-nervous system peptide
 transmitters, defensins, growth factors, vasoactive peptides and
 receptors, binding proteins and malignancy associated proteins. The
 antisense oligonucleotides may be used in this way to treat disorders
 including respiratory obstruction (especially pulmonary obstruction
 and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 2008 BP; 563 A; 463 C; 416 G; 566 T; 0 other;
 Query Match 44.3%; Score 1819.6; DB 21; Length 2008;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 421 AAAAAGTGAAGGTGTAAAGAGCAGACAAAGTGCATTAAGAGATATTTCTCAAAATTTGCCT 480
 Db 150 AAAAAGTGAAGGTGTAAAGAGCAGACAAAGTGCATTAAGAGATATTTCTCAAAATTTGCCT 209
 QY 481 CAAGATGGAACCCCTTTGCCCTCAGGGCATCTTTTGGCTGGCAGCTGGTGGATGTGTAAT 540
 Db 210 CAAGATGGAACCCCTTTGCCCTCAGGGCATCTTTTGGCTGGCAGCTGGTGGATGTGTAAT 269
 QY 541 CAGTGATTAATCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCCACCAC 600
 Db 270 CAGTGATTAATCTGAGAGATACAGCACAAATCTAAGCAATCATGTGGATGATTTCCACCAC 329
 QY 601 TTTTCGTGGCAGAGCTCAGCTTCTCTGTTACCACTCATCAACCCACTAAATTTGGTCT 660
 Db 330 TTTTCGTGGCAGAGCTCAGCTTCTCTGTTACCACTCATCAACCCACTAAATTTGGTCT 389
 QY 661 ACCCAGCAATGGCTCAATGACACACTATPGCCACAGCAGACTAAATTTACTTACGCTTT 720
 Db 390 ACCCAGCAATGGCTCAATGACACACTATPGCCACAGCAGACTAAATTTACTTACGCTTT 449
 QY 721 CAATACATTAACACTGTGATATCTTGTACTATTTTCTGTTGGGAATGGTGGGAATGC 780
 Db 450 CAATACATTAACACTGTGATATCTTGTACTATTTTCTGTTGGGAATGGTGGGAATGC 509
 QY 781 AACTCTGCTCAGGATCATTTTACAGAACAAATGTATAGGAATGCCCCCAACGCCCTGAT 840
 Db 510 AACTCTGCTCAGGATCATTTTACAGAACAAATGTATAGGAATGCCCCCAACGCCCTGAT 569
 QY 841 AGCCAGTCTTGGCCCTTGGAGACCTTATCTATGTGGTCAATGATCTCCCTATCAATGTAT 900
 Db 570 AGCCAGTCTTGGCCCTTGGAGACCTTATCTATGTGGTCAATGATCTCCCTATCAATGTAT 629
 QY 901 TAAGCTCTGGCTGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA 960
 Db 630 TAAGCTCTGGCTGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGTATTTCTTTGCA 689
 QY 961 GCTGTTCCCTTTTTCAGAAAGTCTCGTGGGATACCTCGCTCAACCTCTCGCGCTCT 1020
 Db 690 GCTGTTCCCTTTTTCAGAAAGTCTCGTGGGATACCTCGCTCAACCTCTCGCGCTCT 749
 QY 1021 TAGTGTTCAGAGTACAGAGCAGTTGCTCTCGTGGAGTGTGTTTTCAGGGAATTTGGGATTC 1080
 Db 750 TAGTGTTCAGAGTACAGAGCAGTTGCTCTCGTGGAGTGTGTTTTCAGGGAATTTGGGATTC 809
 QY 1081 TTTGGTGAATGCCATTCGAATTTGCTCCATCTGATCTGCTCTTTTATCTCTGGCCTATTC 1140
 Db 810 TTTGGTGAATGCCATTCGAATTTGCTCCATCTGATCTGCTCTTTTATCTCTGGCCTATTC 869
 QY 1141 TGAAGCATTTGGCTTCGTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1200
 Db 870 TGAAGCATTTGGCTTCGTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 929
 QY 1201 TATGCTCAATGCCACATCAAAATTTTATGAGTGTCTTACCAAGATGTAAAGGACTGGTGCT 1260
 Db 930 TATGCTCAATGCCACATCAAAATTTTATGAGTGTCTTACCAAGATGTAAAGGACTGGTGCT 989
 QY 1261 CTTCCGGGTTCTATTTCTGTATGCTTGGTGTGCGATCTTCTACACCCCTCATGAC 1320

D _b	990	C	T	T	G	G	G	T	T	A	T	T	T	C	T	G	T	A	T	G	C	C	T	T	G	T	G	S	C	A	C	T	G	G	A	T	C	T	T	C	A	C	C	T	C	A	T	G	A	C		104					
Q _y	1321	T	T	G	A	G	A	T	T	G	A	C	A	G	A	A	G	A	T	G	C	A	G	T	T	G	A	A	T	T	G	A	A	T	T	G	C	C	T	C	A	G	T	C	A	G	A	A	C	A	T	C	T	A	A		1380
D _b	1050	T	T	G	A	G	A	T	T	G	A	C	A	G	A	A	G	A	T	G	C	A	G	T	T	G	A	A	T	T	G	A	A	T	T	G	C	C	T	C	A	G	T	C	A	G	A	A	C	T	T	A		1109			
Q _y	1381	G	C	A	G	G	T	C	G	A	G	A	T	T	G	G	C	A	A	A	A	C	A	G	T	T	T	C	T	G	C	T	T	T	T	T	G	T	G	T	A	A	T	T	T	T	T	T	T	T	T	T	T	T		1440	
D _b	1110	G	C	A	G	G	T	C	G	A	G	A	T	T	G	G	C	A	A	A	A	C	A	G	T	T	T	T	C	T	G	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T		1169			
Q _y	1441	G	T	T	C	C	T	C	T	T	C	A	T	T	A	A	G	C	G	T	A	T	T	T	G	A	B	A	A	A	C	T	G	T	A	A	C	G	A	A	A	T	T	A	A	C	A	A	G	A		1500					
D _b	1170	G	T	T	C	C	T	C	T	A	T	T	A	A	G	C	G	T	A	T	T	G	A	B	A	A	A	C	T	G	T	A	A	C	G	A	A	A	T	T	A	A	C	G	A	A	G	A		1229							
Q _y	1501	O	G	A	T	G	A	A	T	T	A	C	T	T	A	G	T	T	T	T	T	C	T	A	C	T	G	C	T	A	T	T	A	C	T	G	G	T	A	T	A	C	T	G	G	T	A	A	C		1560						
D _b	1230	C	G	A	T	G	A	A	T	T	A	C	T	T	A	G	T	T	T	T	T	C	T	A	C	T	G	C	T	A	T	T	A	C	T	G	G	T	A	T	A	C	T	G	G	A	C		1289								
Q _y	1561	C	A	T	G	A	A	T	T	C	A	T	T	A	A	C	C	C	A	T	A	G	C	T	C	T	G	T	A	T	T	T	T	G	A	C	A	A	A	A	T	T	T	A	A	A	A	T	T		1620						
D _b	1290	C	A	T	G	A	A	T	T	C	A	T	T	A	A	C	C	C	A	T	A	G	C	T	C	T	G	T	A	T	T	T	T	G	A	C	A	A	A	A	T	T	T	A	A	A	A	T	T		1349						
D _b	1621	T	T	T	C	A	G	T	C	A	T	G	C	T	C	T	G	T	G	T	T	A	C	C	A	G	T	C	C	A	A	A	A	G	T	C	T	C	A	T	C	A	C	C	T	C	G	T	C	C		1680					
D _b	1350	T	T	T	C	A	G	T	C	A	T	G	C	T	C	T	G	T	T	A	C	C	A	G	T	C	C	A	A	A	A	G	T	C	T	C	A	T	C	A	C	C	T	C	G	T	C	C		1409							
Q _y	1681	C	A	T	G	A	C	G	G	A	C	A	A	G	C	A	T	C	C	A	G	T	G	G	A	A	C	C	A	C	C	A	C	C	A	T	C	A	A	A	A	A	A	C	A	C	A	C		1740							
D _b	1410	C	A	T	G	A	C	G	G	A	C	A	A	G	C	A	T	C	C	A	G	T	G	G	A	A	C																														

RESULT 11

AAA34782
ID AAA34782 standard; DNA: 2008 BP.

AC AAA34782;

EX-100

[illegible]

28-JUL-2000 (first entry)

Human adenosine receptor related polynucleotide SEQ ID NO:2471.

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000

03-AUG-1999: 99WO-IIS17712

03-AUG-1998: 98US-0095212

(UEEC-) UNTV EAST CAROLINA

N₂O TIT.

WPT 2000

100

vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers -

Disclosure; Page 607; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 2008 BP; 563 A; 463 C; 416 G; 566 T; 0 other;

Query Match	44.3%	Score 1819.6;	DB 21;	Length 2008;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1844;	Conservative	0;	Mismatches 4;	Indels 2; Gaps 2;

QY 421 AAAAGTGAAGTGTAAGCAGCACAGTCAATAAGAGATATTCTCAAAATTGCCT 480

Db 150 AAAAGTGAAGGTGTAAGAGCAGCACAGTGCAATAAGAGATATTTCTCAAAATTTGCCCT 209

QV 481 CAAGATGGAAACCCCTTTGGCCCTCAGGGCATCCCTTTTGGCTGGCAGCTGGTGGATGTGTAAT 540

Db	210	 CAAGATGGAAACCCCTTTGGCTCAGGCGATCCCTTTGGCTGGCACTGGTTGGATGTGTAAAT	269
Qy	541	 CAGTGATAATCCTTGAGAGATACAGCAACAATCTAAGCAATCATGTGGATGATTTACCCAC	600
Db	270	 CAGTGATAATCCTTGAGAGATACAGCAACAATCTAAGCAATCATGTGGATGATTTACCCAC	329
Qy	601	 TTTTTCGTGGCAGAGAGCTCAGCTTCCTGGTTACCACCTCATCAACCACCTAAATTTGGTGCCT	660
Db	330	 TTTTTCGTGGCAGAGAGCTCAGCTTCCTGGTTACCACCTCATCAACCACCTAAATTTGGTGCCT	389
Qy	661	 ACCCAGCAATGGCTCAATGCACAACCTATTTCGCCACAGCAGACATAAAATTTACTTCAGCTTT	720
Db	390	 ACCCAGCAATGGCTCAATGCACAACCTATTTCGCCACAGCAGACATAAAATTTACTTCAGCTTT	449
Qy	721	 CAAAATACATTAAACACGTGATATCTTGTAATTTTATCGTGGGAATGGTGGGGAATGC	780
Db	450	 CAAAATACATTAAACACGTGATATCTTGTAATTTTATCGTGGGAATGGTGGGGAATGC	509
Y	781	 AACTCTGCTCAGGATCAATTTACAGAAACAATGTATGAGGAATGGCCCAACGCGCTGAT	840
Db	510	 AACTCTGCTCAGGATCAATTTACAGAAACAATGTATGAGGAATGGCCCAACGCGCTGAT	569
Qy	841	 AGCCAGTCTTGCCCTTGAGAGACCTTATCTPATGTGTGTCATPTGATCTCCCTATCAATGTATT	900
Db	570	 AGCCAGTCTTGCCCTTGAGAGACCTTATCTPATGTGTGTCATPTGATCTCCCTATCAATGTATT	629
Qy	901	 TAAGCTGCTGGCTGGCGCTGGCCCTTTTGATCACAATGACATTTGGCGTATTTCTTTGCAG	960
Db	630	 TAAGCTGCTGGCTGGCGCTGGCCCTTTTGATCACAATGACATTTGGCGTATTTCTTTGCAG	689
Qy	961	 GCTGTTCCTCTTTTTCAGAAAGTCTCGGTGGGGATCACCGTCTCAACCTCTCGCGCTCT	1020
Db	690	 GCTGTTCCTCTTTTTCAGAAAGTCTCGGTGGGGATCACCGTCTCAACCTCTCGCGCTCT	749
Qy	1021	 TAGTGTTCAGAGTACAGACAGTTCGCTCTCTGGAGTCTGTTTCAGGGAATTTGGGATTC	1080
Db	750	 TAGTGTTCAGAGTACAGACAGTTCGCTCTCTGGAGTCTGTTTCAGGGAATTTGGGATTC	809
Qy	1081	 TTTGGTAACTGCCATTGAAATTTGCTCCATCTGGATCTGTCCTTTATCTCTGGCCATTC	1140
Db	810	 TTTGGTAACTGCCATTGAAATTTGCTCCATCTGGATCTGTCCTTTATCTCTGGCCATTC	869
Qy	1141	 TGAAGCGATTGGCTTCGTCATCGTACCCCTTTTGAATATATAGGGGTGAACAGCATAAACCTG	1200
Db	870	 TGAAGCGATTGGCTTCGTCATCGTACCCCTTTTGAATATATAGGGGTGAACAGCATAAACCTG	929
Y	1201	 TATGCTCAATGGCCACATCAAAATTCATGAGTTCTTACCAAGATGTAAGGACTTGGTGGCT	1260
Db	930	 TATGCTCAATGGCCACATCAAAATTCATGAGTTCTTACCAAGATGTAAGGACTTGGTGGCT	989
Qy	1261	 CTTCGGGTCTATTTCTGTATGCCCTGGCTGGCACTCGGATCTTCTACACCCTCATGAC	1320
Db	990	 CTTCGGGTCTATTTCTGTATGCCCTGGCTGGCACTCGGATCTTCTACACCCTCATGAC	1049
Qy	1321	 TTGTGAGATGTTGAACAGAGAAGTAATTCAGAAACACTCTGTATTAACCAATGACACAGAA	1380
Db	1050	 TTGTGAGATGTTGAACAGAGAAGTAATTCAGAAACACTCTGTATTAACCAATGACACAGAA	1109
Qy	1381	 GCAGCGTCCAGAAAGTGGCAAAACAGTTTCTGCTTGGTTGTAAATTTTTCCTTTGGCTG	1440
Db	1110	 GCAGCGTCCAGAAAGTGGCAAAACAGTTTCTGCTTGGTTGTAAATTTTTCCTTTGGCTG	1169
Qy	1441	 GTTCCCTCTTCACTTAAAGCGGTATATTCAGAAACACTCTGTATTAACCAATGACACAGAA	1500
Db	1170	 GTTCCCTCTTCACTTAAAGCGGTATATTCAGAAACACTCTGTATTAACCAATGACACAGAA	1229
Qy	1501	 CCGATGTGAATTTACTTAGTTTCTTACTGCTCATGGATTCATCGGTATTAACCTTGGCAAC	1560
Db	1230	 CCGATGTGAATTTACTTAGTTTCTTACTGCTCATGGATTCATCGGTATTAACCTTGGCAAC	1289
Qy	1561	 CATGAAATTCATATAAACCCCATAGCTCTGTATTTTGTGACGAGAAGAAATTTAAAAATTG	1620

Db	1290	CATGAAATTCATGTAATAAACCCCATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATTCG	1349
Qy	1621	TTTCCAGTCATGCCTCTGCTGCTGTGTTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1680
Db	1350	TTTCCAGTCATGCCCTGCTGCTGTGTTTACCAGTCCAAAAGTCTGATGACCTCGGTCCC	1409
Qy	1681	CATGAACGGAACAAGCATCCAGTGGGAAGAACCAACACGATCAAAACAACCAACACACACCG	1740
Db	1410	CATGAACGGAACAAGCATCCAGTGGGAAGAACCAACACGATCAAAACAACCAACACACACCG	1469
Qy	1741	GAGCAGCCATAAGGACAGCATGAACCTGACCAACCCCTTAGAAGCACTCCTCGGTACTCCCAT	1800
Db	1470	GAGCAGCCATAAGGACAGCATGAACCTGACCAACCCCTTAGAAGCACTCCTCGGTACTCCCAT	1529
Qy	1801	AATCCTCTCGGAGAAAAAATCACAAAGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Db	1530	AATCCTCTCGGAGAAAAAATCACAAAGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1589
Qy	1861	CTTCTTCCTTAATTCACCTCCCAACCCCAAGAAAGAAATGCTTTTCCAAAACCGCAA -GGTAG	1919
Db	1590	CTTCTTCCTTAATTCACCTCCCAACCCCAAGAAAGAAATGCTTTTCCAAAACCGCAAGGTAG	1649
Qy	1920	ACTGGTTATCCACCACACACATCTACGAATCGTACTTCTTTAAATTGATCTAATTTACAT	1979
Db	1650	ACTGGTTATCCACCACACACATCTACGAATCGTACTTCTTTAAATTGATCTAATTTACAT	1709
Qy	1980	ATTCGCGGTGTGATTACGACACTAAAATAATGGTGGAGCTGGGGAGAATGAAGACTGT	2039
Db	1710	ATTCGCGGTGTGATTACGACACTAAAATAATGGTGGAGCTGGGGAGAATGAAGACTGT	1769
Qy	2040	TAAATGAACACAGAGGATATTACTACTTTTGCATGAAAAATAGAGCTTTTCAAGTACATG	2099
Db	1770	TAAATGAACACAGAGGATATTACTACTTTTGCATGAAAAATAGAGCTTTTCAAGTACATG	1829
Qy	2100	GCTAGCTTTTATGGCAGTCTCGGTGAATGTTCAATGGGAACGGTCACCATGAACCTTTA	2159
Db	1830	GCTAGCTTTTATGGCAGTCTCGGTGAATGTTCAATGGGAACGGTCACCATGAACCTTTA	1889
Qy	2160	GAGATTACGACAACATTTCTACTTTTTTAAAGTGA -TTTTTTCGTCCTTCAGCCAAACA	2218
Db	1890	GAGATTACGACAACATTTCTACTTTTTTAAAGTGAATTTTTTGTGCTTCAGCCAAACA	1949
Qy	2219	CAATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTAT 2268	
Db	1950	CAATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTAT 1999	
RESULT 12			
AAF21447			
ID	AAF21447	standard; DNA; 5036 Bp.	
XX	AC	AAF21447;	
XX	DT		
XX	DE	14-MAR-2001 (first entry)	
XX	XX	Human endothelin receptor A polynucleotide fragment #3014.	
KW	KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;	
KW	KW	human; airway disorder; bronchoconstriction; lung inflammation;	
KW	KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;	
KW	KW	immunosuppressive; antialsthmatic; analgesic; hypotensive; cytostatic;	
KW	KW	respiratory obstruction; pulmonary vasoconstriction; impeded respiration;	
KW	KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;	
KW	KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;	
KW	KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;	
KW	KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;	
XX	XX	cancer; ss.	
OS	OS	Homo sapiens.	
XX	PN		
XX	PD	WO200062736-A2.	
XX	DD	26-OCT-2000.	

	24-MAR-2000; 2000WO-US08020.
	06-APR-1999; 99US-0127958.
	(UYEC-) UNIV EAST CAROLINA.
	(NYCE/) NYCE J.W.
	Nyce JW;
	WPI; 2000-679539/66.
	Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
	Disclosure; Page 243-244; 1592pp; English.
	The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (ARDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.
	Sequence 5036 BP; 1359 A; 1148 C; 1060 G; 1469 T; 0 other;
	Query Match 44.3%; Score 1819, 6; DB 21; Length 5036;
	Best Local Similarity 99.7%; Pred. No. 0;
	Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps
Qy	421 AAAAAGTGAAGGTGTAAGAAGCAGCACAAAGTCGAATAAGAGATATTCTCAAATTTGCCT 480
Db	1310 AAAAAGTGAAGGTGTAAGAAGCAGCACAAAGTCGAATAAGAGATATTCTCAAATTTGCCT 1369
Qy	481 CAAGATGAAACCCCTTTGGCCTCAGGCCATCCTTTTGGCTGGCATCGTTGGATGTGTAAT 540
Db	1370 CAAGATGAAACCCCTTTGGCCTCAGGCCATCCTTTTGGCTGGCATCGTTGGATGTGTAAT 1429
Qy	541 CAGTGTAATCCTCAGAGATACACACAATACTAAGCAATCATCTGGATGATTTCCACCAC 600
Db	1430 CAGTGTAATCCTCAGAGATACACACAATACTAAGCAATCATCTGGATGATTTCCACCAC 1489
Qy	601 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTTACCACACTCATCAACCCCACTAATTTGGTCCT 660
Db	1490 TTTTCGTGGCACAGAGCTCAGCTTCCTGGTTTACCACACTCATCAACCCCACTAATTTGGTCCT 1549
Qy	661 ACCGAGCAATGGCTCAATGCACAACACTATGTCCCCACAGCAGACTAAAAATTACTCAGCTTT 720
Dp	1550 ACCGAGCAATGGCTCAATGCACAACACTATGTCCCCACAGCAGACTAAAAATTACTCAGCTTT 1609

QY 1801 AATCCTCTCGGAGAAAAAATCACAAGGCACTGTGACTCGGGAATCTTCTCTGATC 1860
Db AATCCTCTCGGAGAAAAAATCACAAGGCACTGTGACTCGGGAATCTTCTCTGATC 2749
QY 1861 CTCTCTCTTAATTAATCACTCCACACCAAGAGAAATGCTTCCAAACCCCAAGGTA 1919
Db CTCTCTCTTAATTAATCACTCCACACCAAGAGAAATGCTTCCAAACCCCAAGGTA 2809
QY 1920 ACTGGTTTATCCACCAACATCTCGAATCGTACTTCTTAAATGATCTAAATTTACAT 1979
Db ACTGGTTTATCCACCAACATCTCGAATCGTACTTCTTAAATGATCTAAATTTACAT 2869
QY 1980 ATTCTGGTGTGTTATTCAGACATAAATAATGTTGGGAGCTGGGGAGAAATGAAGACTGT 2039
Db ATTCTGGTGTGTTATTCAGACATAAATAATGTTGGGAGCTGGGGAGAAATGAAGACTGT 2929
QY 2040 TAAATGAACCAAGAGATATTTACTACTTTTGTGATGAATAAGACTTCAAGTACATG 2099
Db TAAATGAACCAAGAGATATTTACTACTTTTGTGATGAATAAGACTTCAAGTACATG 2989
QY 2100 GCTAGCTTTTATGGCAGTCTGTTGGAATGTTCAATGGGAATGCTCACCATGAACCTTTA 2159
Db GCTAGCTTTTATGGCAGTCTGTTGGAATGTTCAATGGGAATGCTCACCATGAACCTTTA 3049
QY 2160 GAGATTAAACGACAGATTTTCTACTTTTAAAGTGA-TTTTTGTCTCTCAGGCCAACA 2218
Db GAGATTAAACGACAGATTTTCTACTTTTAAAGTGA-TTTTTGTCTCTCAGGCCAACA 3109
QY 2219 CAATATGGGCTCAGGTCACCTTTATTTGAATGTCATTTGGTGCCAGTAT 2268
Db CAATATGGGCTCAGGTCACCTTTATTTGAATGTCATTTGGTGCCAGTAT 3159
RESULT 13
AAF21435
ID AAF21435 standard; DNA; 117609 BP.
XX AC AAF21435;
XX AC AAF21435;
-DT 14-MAR-2001 (first entry)
XX Human receptor-related antisense polynucleotide #3002.
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
-KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; anti-inflammatory;
KW immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;
-W respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
cancer; ss.
XX Homo sapiens.
XX OS
XX W0200062736-A2.
XX PN
XX 26-OCT-2000.
XX PD
XX 24-MAR-2000; 2000MO-US08020.
XX PF
XX 06-APR-1999; 99US-0127958.
XX PR
XX (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX PA
XX NYCE JW;
XX PI
XX WPI; 2000-679539/66.
DR WPI; 2000-679539/66.
XX WPI; 2000-679539/66.
XX WPI; 2000-679539/66.
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating

Cancers and respiratory obstructions -

Disclosure; Page 17-47; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, anti-inflammatory, analgesic,
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hyperinflation, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

SQ Sequence 117609 BP; 27530 A; 29942 C; 30320 G; 29441 T; 376 other;

Query Match

Best Local Similarity 44.3%; Score 1819.6; DB 21; Length 117609;

Matches 1844; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 421 AAAAGTGAAGGTGTAAGAGCAGCACAAGTGAAGAGATTTTCTCAAAATTTGCCT 480
Db 87367 AAAAGTGAAGGTGTAAGAGCAGCACAAGTGAAGAGATTTTCTCAAAATTTGCCT 87426
QY 481 CAAGTGAAGACCTTTTGGCTCAGGCATCTTTTGGCTGGCAGCTGGTGGATGTAAT 540
Db 87427 CAAGTGAAGACCTTTTGGCTCAGGCATCTTTTGGCTGGCAGCTGGTGGATGTAAT 87486
QY 541 CAGTGATATCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCCACCAC 600
Db 87487 CAGTGATATCTGAGAGATACAGCACAATCTAAGCAATCATGTGGATGATTTCCACCAC 87546
QY 601 TTTTGGTGACAGAGCTCAGCTTCTGTTTACCACCTCATCAACCACCTAAATTTGCTCT 660
Db 87547 TTTTGGTGACAGAGCTCAGCTTCTGTTTACCACCTCATCAACCACCTAAATTTGCTCT 87606
QY 661 ACCAGCAATGGCTCAATGCCACAATATTTGCCACAGCAGACTAAATTTACTTCAGCTTT 720
Db 87607 ACCAGCAATGGCTCAATGCCACAATATTTGCCACAGCAGACTAAATTTACTTCAGCTTT 87666
QY 721 CAATACATTAACACTGTGATATCTTGTACTATTTTTCATCGTGGGAATGGTGGGAATGC 780
Db 87667 CAATACATTAACACTGTGATATCTTGTACTATTTTTCATCGTGGGAATGGTGGGAATGC 87726
QY 781 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACCGCTGAT 840
Db 87727 AACTCTGCTCAGGATCATTTTACCAGAACAAATGTATGAGGAATGGCCCCAACCGCTGAT 87786
QY 841 AGCCAGTCTTGGCTTGGAGACCTTATCTATGTGTGATGATCTCCCTATCAATGATTT 900
Db 87787 AGCCAGTCTTGGCTTGGAGACCTTATCTATGTGTGATGATCTCCCTATCAATGATTT 87846
QY 901 TAAGTCTGCTGGCTGGGCTGGCCTTTTGCATCACAATGACTTTGGCGTATTTTGGCAA 960

Db	87847	TAAGCTGTGCGTGGCGCGCTGGCCCTTTTGATCACAAATGACATTGGCGGTATTTCTTTGGCAA	87906
Qy	961	GCTGTTCCCTTTTGTGCAGAAAGTCTCGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	1020
Db	87907	GCTGTTCCCTTTTGTGCAGAAAGTCTCGTGGGGATCACCGTCCTCAACCTCTGCGCTCT	87966
Qy	1021	TAGTGTGCACAGGTACAGAGCAGTTGCCCTCCTGGAGTCGTGTTCAGGGAATTTGGGATTCC	1080
Db	87967	TAGTGTGCACAGGTACAGAGCAGTTGCCCTCCTGGAGTCGTGTTCAGGGAATTTGGGATTCC	88026
Qy	1081	TTTGGTAACTGCCATTGAAATTTGCTCACTGGATCCTGCTCTTATCTTGGCCATTCC	1140
Db	88027	TTTGGTAACTGCCATTGAAATTTGCTCACTGGATCCTGCTCTTATCTTGGCCATTCC	88086
Qy	1141	TGAAGCGATTGGCTTCGTCATGGTACCCCTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
Db	88087	TGAAGCGATTGGCTTCGTCATGGTACCCCTTTGAATATAGGGGTGAACAGCATAAACCTG	88146
Qy	1201	TATGCTCAATGCCACATCAAAATTCATGGAGTTCCTACCAAGATGTAAGGACTGGTGGCT	1260
Db	88147	TATGCTCAATGCCACATCAAAATTCATGGAGTTCCTACCAAGATGTAAGGACTGGTGGCT	88206
Qy	1261	CTTCCGGTTCTATTTCCTGTATGCCCTTGGTGTGCACATGCGATCTTACACCCCTCATGAC	1320
Db	88207	CTTCCGGTTCTATTTCCTGTATGCCCTTGGTGTGCACATGCGATCTTACACCCCTCATGAC	88266
Qy	1321	TTGTGAGATGTTGAACAGAGGAATGCGAGCTTCAGAAATTCGCCCTCAGTGAACATCTTAA	1380
Db	88267	TTGTGAGATGTTGAACAGAGGAATGCGAGCTTCAGAAATTCGCCCTCAGTGAACATCTTAA	88326
Qy	1381	GCAGCGTCGAGAAAGTGGCAAAACAGTTTCTGCTGGTTGTAAATTTGCTCTTTGCTG	1440
Db	88327	GCAGCGTCGAGAAAGTGGCAAAACAGTTTCTGCTGGTTGTAAATTTGCTCTTTGCTG	88386
Qy	1441	GTTCCTCTTCACHTTAAGCCGTATATTGAAGAAACHTGTGTAAACGAAATGGACAAGAA	1500
Db	88387	GTTCCTCTTCATTTAAGCCGTATATTGAAGAAACHTGTGTAAACGAGATGGACAAGAA	88446
Qy	1501	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTTGGCAAC	1560
Db	88447	CCGATGTGAATTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTTGGCAAC	88506
Qy	1561	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTGTGAGCAAGAAATTTAAAAATTG	1620
Db	88507	CATGAATTCATGTATAAACCCCATAGCTCTGTATTTGTGAGCAAGAAATTTAAAAATTG	88566
Qy	1621	TTTCCAGTCATGCTGCTGCTGTACCAGTCCAAAGTCTGATGACTCGGTGCC	1680
Db	88567	TTTCCAGTCATGCTGCTGCTGTACCAGTCCAAAGTCTGATGACTCGGTGCC	88626
Qy	1681	CATGAACGGAACAAAGCATCCAGTGGGAAGAACACAGATCAAAACCAACACACAGACCG	1740
Db	88627	CATGAACGGAACAAAGCATCCAGTGGGAAGAACACAGATCAAAACCAACACACAGACCG	88686
Qy	1741	GAGCAGCCATAAGCAGCAGATGAACATGACACCCCTTAGAGACTCTCTCGGTACTCCCAT	1800
Db	88687	GAGCAGCCATAAGCAGCAGATGAACATGACACCCCTTAGAGACTCTCTCGGTACTCCCAT	88746
Qy	1801	AATPCTCTCGGAGAAAAATACAGGCAACTGTGACTCCGGGAATCTCTCTGTATC	1860
Db	88747	AATPCTCTCGGAGAAAAATACAGGCAACTGTGACTCCGGGAATCTCTCTGTATC	88806
Qy	1861	CTTCTTCCCTTAATTCATCTCCACACCCAAAGAAATGCTTTCCAAAAACCGCAA -GGTAG	1919
Db	88807	CTTCTTCCCTTAATTCATCTCCACACCCAAAGAAATGCTTTCCAAAAACCGCAAGGTAG	88866
Qy	1920	ACTGGTTTATCCACCACACATCTACGAATCGTACTCTTTAAATGATCTAATTTACAT	1979
Db	88867	ACTGGTTTATCCACCACACATCTACGAATCGTACTCTTTAAATGATCTAATTTACAT	88926
Qy	1980	ATTCTCGGTGTATTTCAGCACTAAAAAATGGTGGGAGATGAAGACTGT	2039

Db	88927	ATTCTCGGTGTTGTTATT	CAGCACTAAAAAATGGTGGGAGCTGGGGGAGAAATCAAGACTGT	88988
QY	2040	TAATGAAACACAGAAGGATATT	TACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG	2099
Db	88987	TAATGAAACACAGAAGGATATT	TACTACTTTTGCATGAAATAGAGCTTTCAAGTACATG	89046
QY	2100	GCTAGCTTTTATGGCAGTCT	GGTGAATGTTCAATGGGAACCTGGTCAACCATGAAACTTTTA	2159
Db	89047	GCTAGCTTTTATGGCAGTCT	GGTGAATGTTCAATGGGAACCTGGTCAACCATGAAACTTTTA	89106
QY	2160	GAGATTACGACACAGATT	TTCTACTTTTTTAAAGTGA-TTTTTGTCTCTCAGCCAAACA	2218
Db	89107	GAGATTACGACACAGATT	TTCTACTTTTTTAAAGTGA-TTTTTGTCTCTCAGCCAAACA	89166
QY	2219	CAATATGGGCTCAGTCACT	TTTTTATTCGAAATGTCATTTGGTGGCAGTAT	2268
Db	89167	CAATATGGGCTCAGTCACT	TTTTTATTCGAAATGTCATTTGGTGGCAGTAT	89216
RESULT	14			
ID	AAF20902			
XX	AAF20902	standard; DNA; 1310 BP.		
AC	AAF20902;			
XX	14-MAR-2001	(first entry)		
XX	Human endothelin receptor A	polynucleotide fragment #2469.		
KW	Low adenosine antisen-	se oligonucleotide; phosphorothioate; allergy;		
KW	human; airway disorder;	bronchoconstriction; lung inflammation;		
KW	surfactant depletion;	respiratory; bronchodilator; antiinflammatory;		
KW	immunosuppressive;	antialsthmatic; analgesic; hypotensive; cytostatic;		
KW	respiratory obstruction;	pulmonary obstruction; impeded respiration;		
KW	resistant hypoproduction;	pulmonary vasoconstriction; asthma; RDS;		
KW	respiratory distress syndrome;	pain; cystic fibrosis; allergic rhinitis		
KW	pulmonary hypertension;	emphysema; pulmonary transplantation rejection;		
KW	chronic obstructive pulmonary	disease; pulmonary infection; bronchitis;		
KW	cancer; ss.			
XX	XX			
OS	Homio sapiens.			
XX	XX			
PN	WO200062736-A2.			
XX	XX			
PD	26-OCT-2000.			
XX	XX			
PF	24-MAR-2000; 2000WO-US08020.			
XX	XX			
PR	06-APR-1999; 99US-0127958.			
XX	XX			
PA	(UYEC-) UNIV EAST CAROLINA.			
PA	(NYCE/) NYCE J W.			
XX	XX			
PI	Nyce JW;			
XX	XX			
DR	WPI; 2000-679539/66.			
XX	XX			
PT	Low adenosine (A) content	antisense oligonucleotides which do not		
PT	trigger adenosine receptors	during metabolism, useful e.g. for treating		
PT	cancers and respiratory ob-	structions -		
XX	XX			
PS	Disclosure; Page 244-245;	1592pp; English.		
XX	XX			
CC	The present invention descri-	bes low adenosine (A) content antisense		
CC	oligonucleotides and composi-	tions (I) comprising them. In the antisense		
CC	oligonucleotides the A is re-	placed by a 'Universal' or alternative base.		
CC	(I) can have respiratory, bron-	chodilator, antiinflammatory, analgesic,		
CC	immunosuppressive, antialstha-	matic, hypotensive and cytostatic activities.		
CC	The antisense oligonucleotides	and (I) can be used to down-regulate the		
CC	expression and or activity of	target polypeptides associated with		
CC	lung/respiratory disorders and	malignancies, such as stimulating and		
CC	activating peptide factors and	transmitters, transcription factors,		
CC	immunoglobulins and antibodies,	antibody receptors, cytokines and		

CC Chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergies (ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.

AX
 SQ Sequence 1310 BP; 337 A; 312 C; 284 G; 377 T; 0 other;

Query Match 31.6%; Score 1296.8; DB 21; Length 1310;
 Best Local Similarity 99.3%; Pred. No. 1.7e-303;
 Matches 1301; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY	481	CAAGATGGAAACCTTTGGCTCAGGGCATCCTTTGGCTGGCAGCTGGTGGATGTAAT	540
DB	3	CACATGGAAACCTTTGGCTCAGGGCATCCTTTGGCTGGCAGCTGGTGGATGTAAT	62
QY	541	CAGTGATAATCCTGAGAGATACAGCAAAATCTAAGCAATCATCTGGATGATTTCAACAC	600
DB	63	CAGTGATAATCCTGAGAGATACAGCAAAATCTAAGCAATCATCTGGATGATTTCAACAC	122
QY	601	TTTTCTGGGCACAGAGCTCAGCTCTCTGGTTACCACTCATCAACCCACTAAATTTGGTCT	660
DB	123	TTTTCTGGGCACAGAGCTCAGCTCTCTGGTTACCACTCATCAACCCACTAAATTTGGTCT	182
QY	661	ACCAGCAATGGCTCAATGACACAACTATGCCCACACAGACTAAATTTACTTACGCTTT	720
DB	183	ACCAGCAATGGCTCAATGACACAACTATGCCCACACAGACTAAATTTACTTACGCTTT	242
QY	721	CAATACATTAACACTGTGATATCTTCTACTATTTTCTGTTGGAATGGTGGGAATGC	780
DB	243	CAATACATTAACACTGTGATATCTTCTACTATTTTCTGTTGGAATGGTGGGAATGC	302
QY	781	AATCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	840
DB	303	AATCTGCTCAGGATCATTTACCAGAACAAATGTATGAGGAATGGCCCCAACGCGCTGAT	362
QY	841	AGCCAGTCTTGGCCCTGGAGACCTTATCTATGTGGTCAATGATCCCTATCAATGATTT	900
DB	363	AGCCAGTCTTGGCCCTGGAGACCTTATCTATGTGGTCAATGATCCCTATCAATGATTT	422
QY	901	TAAGCTGCTGGCTGGCGCTGGCTTTTGATACAAAGTCTTTGGCGCTATTTCTTTCGAA	960
DB	423	TAAGCTGCTGGCTGGCGCTGGCTTTTGATACAAAGTCTTTGGCGCTATTTCTTTCGAA	482
QY	961	GCCTGTTCCCTTTTTCAGAAAGCTCTCGGGGGGATCACCGTCTCAACCTCTCGCTCT	1020
DB	483	GCCTGTTCCCTTTTTCAGAAAGCTCTCGGGGGGATCACCGTCTCAACCTCTCGCTCT	542
QY	1021	TAGTGTGACAGGTACAGACAGTTGCTCTCTGGAGTGGTGTTCAGGGAATTTGGGATTC	1080
DB	543	TAGTGTGACAGGTACAGACAGTTGCTCTCTGGAGTGGTGTTCAGGGAATTTGGGATTC	602
QY	1081	TTTGGTAACCTGCCATGAATTTGCTCCATCTGGATCTGCTCTTTATCTGGCCATTC	1140
DB	603	TTTGGTAACCTGCCATGAATTTGCTCCATCTGGATCTGCTCTTTATCTGGCCATTC	662
QY	1141	TGAAGGATTTGGCTTCGCTCATGTGTACCTTTTGAATATAGGGGTGAACAGCATAAACCTG	1200
DB	663	TGAAGGATTTGGCTTCGCTCATGTGTACCTTTTGAATATAGGGGTGAACAGCATAAACCTG	722

QY	1201	TATGCTCAATGCCACATCAAAATTCATGAGTTCACCAAGATGTAAAGACTGGTGGCT	1260
DB	723	TATGCTCAATGCCACATCAAAATTCATGAGTTCACCAAGATGTAAAGACTGGTGGCT	782
QY	1261	CTTGGGTTCTATTTCTGTATGCCCCCTGGTGGCACTGGGATCTTCTACACCTCATGAC	1320
DB	783	CTTGGGTTCTATTTCTGTATGCCCCCTGGTGGCACTGGGATCTTCTACACCTCATGAC	842
QY	1321	TTGTGAGATGTTGAACAGGAAGTAATGGCAGCTTGAGAATTTGCCCTCAGTGAACATCTTA	1380
DB	843	TTGTGAGATGTTGAACAGGAAGTAATGGCAGCTTGAGAATTTGCCCTCAGTGAACATCTTA	902
QY	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTCTGCTTGGTGTGAATTTTTCCTTTGCTG	1440
DB	903	GCAGCGTCGAGAAGTGGCAAAACAGTTTCTGCTTGGTGTGAATTTTTCCTTTGCTG	962
QY	1441	GTTCCCTCTTCACTTAAGCCGTATATTTGAAGAAAACCTGTGTATTAACGAGATGGACAAG	1500
DB	963	GTTCCCTCTTCACTTAAGCCGTATATTTGAAGAAAACCTGTGTATTAACGAGATGGACAAG	1022
QY	1501	CCGATGTGAATTAATTTCTTACTGCTCATGATTAACATCGGTATTAACCTTGGCAAC	1560
DB	1023	CCGATGTGAATTAATTTCTTACTGCTCATGATTAACATCGGTATTAACCTTGGCAAC	1082
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QY	1621	TTTCCAGTCATGCTCTGCTGTGTATTTACCAAGTCCAAAACCTGTGATGACCTCGTCC	1680
DB	1143	TTTCCAGTCATGCTCTGCTGTGTATTTACCAAGTCCAAAACCTGTGATGACCTCGTCC	1202
QY	1681	CATGAACGGAAACAGATCCAGTGGAGAACCAACCATCAAAACCAACCAACAGACCG	1740
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RESULT 15

AAF20914
 ID AAF20914 standard; DNA; 1310 BP.

XX AAF20914;

XX 14-MAR-2001 (first entry)

XX Human ELAM-1 polynucleotide fragment #2481.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cycostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

OS OS

PN WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

XX 06-APR-1999; 99US-0127958.

XX

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2002, 09:25:42 ; Search time 10083 Seconds
(without alignments)
11848.360 Million cell updates/sec

Title: US-09-931-157-1
Perfect score: 4105
Sequence: 1 gaattcgccgcgcctcttg.....taaaagttacagaaacctt 4105

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

arched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Result No.	Score	Query Match %	Length	DB ID	Description
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2	4105	100.0	4105	6	E07649 cDNA encodi
3	4105	100.0	4105	9	X61950 H.sapiens m
4	4103	100.0	4105	9	S57498 endothelin
5	4101	99.9	4101	9	D90348 Human mRNA
6	3183.2	77.5	3305	9	S45956 endothelin
7	2609.6	63.6	2705	9	BC022511 Homo sapi
8	2470	60.2	2595	9	D1151 Human DNA f
9	2409.2	58.7	164920	9	AC093908 Homo sapi
10	2292	55.8	2337	11	G06463 human STS W
11	1819.6	44.3	1868	9	S63938 A-type endo
12	1786.6	43.5	3216	4	BTBETREC
13	1560.2	38.0	1661	9	S67127 Bovine mRNA
14	1359	33.1	1359	9	S81539
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20	1048.8	25.5	1180	4	AF311974
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22	997	24.3	1436	10	RATENDOR
23	951	23.2	1160	9	S81542
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25	765.8	18.7	2988	5	AF472618 Gallus ga
26	695	16.9	1032	9	S81545
27	632.8	15.4	1650	5	XL006633 Xenopus lae
28	624.6	15.2	810	10	AF039892 Mus muscu
29	514	12.5	530	9	MF020577
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31	487.4	11.9	1435	9	S55547S2
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33	425	10.4	1308	5	CCEDNRB2
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35	411.6	10.0	1724	5	AB045356
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39	406.2	9.9	1321	6	AR207426
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41	403.8	9.8	1965	6	E03623
42	403.8	9.8	2018	10	S65355
43	403	9.8	1326	4	AF245469
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45	402.4	9.8	1564	5	AF472616

ALIGNMENTS

RESULT 1
AR177879
LOCUS AR177879
DEFINITION Sequence 1 from patent US 6313276.
ACCESSION AR177879
VERSION AR177879.1 GI:17920234
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4105)
AUTHORS Imura,H., Nakao,K. and Nakanishi,S.
TITLE Human endothelin receptor
JOURNAL Patent: US 6313276-A 1 06-NOV-2001;
FEATURES Location/Qualifiers

AR177879 Sequence 1 from patent US 6313276.
4105 bp DNA linear PAT 17-DEC-2001

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Best Local Similarity	100.0%; Pred. No. 0;
Matches 4105; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Dd	
Db	1 GAATTCGGCGGCGCTCTTTGGGTCCACAGATGGAGTGAAGGTCTGCAGCTTTGGGAGG 60
Qy	61 AGACGGGAGGACAGACTTGAGGGGTGTTCTCCGGAGTTTTCTTTTCGTGCGAGCCTT 120
Dd	
Db	61 AGACGGGAGGACAGACTTGAGGGGTGTTCTCCGGAGTTTTCTTTTCGTGCGAGCCTT 120
Qy	121 CGCGGCCGTACAGTCAATCCGCTGGTCTCACGATTGTGAGAGGGCGGTGAGAGGCTT 180
Dd	
Db	121 CGCGGCCGTACAGTCAATCCGCTGGTCTCACGATTGTGAGAGGGCGGTGAGAGGCTT 180
Qy	181 CATCATCCCCACC GGTCGTGCGCGGGGATTTGGGTCCACGACACACTCCC CGGAGAA 240
Dd	
Db	181 CATCATCCCCACC GGTCGTGCGCGGGATTTGGGTCCACGACACACTCCC CGGAGAA 240
Qy	241 GCAGTGGCCAGGAAGTTTTCTGAACCGGGGAAAGCTGTGCAGCCGAAGCCGCCCGCGGC 300
Dd	
Db	241 GCAGTGGCCAGGAAGTTTTCTGAACCGGGGAAAGCTGTGCAGCCGAAGCCGCCCGCGGC 300
Qy	301 CGGAGCCGGGACACCGGCCACCTTCGCGGCCACCCACCCTTCGCTTTC CGGCTTCC 360
Dd	
Db	301 CGGAGCCGGGACACCGGCCACCTTCGCGGCCACCCACCCTTCGCTTTC CGGCTTCC 360
Qy	361 TGGCCAGCGCCGCGGACCGGACCTGTCTGCGCACCGCAGCTCCACGCTGA AAA 420
Dd	
Db	361 TGGCCAGCGCCGCGGACCGGACCTGTCTGCGCACCGCAGCTCCACGCTGA AAA 420
Qy	421 AAAAAAGTGAAGGTGTAAAAGCAGACAAGTGCATAAGAGATATTTCTCAAATTTGGCT 480
Dd	
Db	421 AAAAAAGTGAAGGTGTAAAAGCAGACAAGTGCATAAGAGATATTTCTCAAATTTGGCT 480
Qy	481 CAAGATGAAAACCCCTTTGCCCTCAGGGCATCTTTTGGCTGGCACTGGTTGGATGTGAAT 540
Dd	
Db	481 CAAGATGAAAACCCCTTTGCCCTCAGGGCATCTTTTGGCTGGCACTGGTTGGATGTGAAT 540
Qy	541 CAGTGAATACTCTGAGAGATACAGACAAAATCTAAGCAATCATCTGGATGATTTTCAACC 600
Dd	
Db	541 CAGTGAATACTCTGAGAGATACAGACAAAATCTAAGCAATCATCTGGATGATTTTCAACC 600
Qy	601 TTTTCGTGGCACAGAGCTCAGCTTCCCTGGTTTACACATCATCAACCCACTAATTTGGTCT 660
Dd	
Db	601 TTTTCGTGGCACAGAGCTCAGCTTCCCTGGTTTACACATCATCAACCCACTAATTTGGTCT 660
Qy	661 ACCAGCAATGGCTCAATGCAAACTATTGCCACAGCAGACTAAAATTA CTTCAGCTTT 720
Dd	
Db	661 ACCAGCAATGGCTCAATGCAAACTATTGCCACAGCAGACTAAAATTA CTTCAGCTTT 720
Qy	721 CAATACATTAACACTGTGATATCTTGATATATTTTCATCGTGGGAATG GTGGGAATGC 780
Dd	
Db	721 CAATACATTAACACTGTGATATCTTGATATATTTTCATCGTGGGAATG GTGGGAATGC 780
Qy	781 AACTCTGCTAGGATCATTTACAGAACAAATGTATAGGAATGGCCCCAACCGCGCTGAT 840
Dd	
Db	781 AACTCTGCTAGGATCATTTACAGAACAAATGTATAGGAATGGCCCCAACCGCGCTGAT 840
Qy	841 AGCCAGCTTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGATTT 900
Dd	
Db	841 AGCCAGCTTTGCCCTTGGAGACCTTATCTATGTGGTCATTGATCTCCCTATCAATGATTT 900
Qy	901 TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGCTATTTCTTGCAA 960
Dd	
Db	901 TAAGCTGCTGGCTGGGCGCTGGCCCTTTTGATCACAATGACTTTGGCGCTATTTCTTGCAA 960

Db	2041	AAATGAAACGACGAAGGATATTTACTACTTTTGCATGAAAATAGAGCTTTCAGTACATGG	2100
Qy	2101	CTAGCTTTTATGGCAGTCTCTGGTGAATGTTCAATGGGAACGGTCAACATGAACATTTAG	2160
Db	2101	CTAGCTTTTATGGCAGTCTCTGGTGAATGTTCAATGGGAACGGTCAACATGAACATTTAG	2160
Qy	2161	AGATTAAACGACAAAGATTTTCTACTTTTTTAAAGTGATTTTTTGTCTCCTCAGCCAAACACA	2220
Db	2161	AGATTAAACGACAAAGATTTTCTACTTTTTTAAAGTGATTTTTTGTCTCCTCAGCCAAACACA	2220
Qy	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Db	2221	ATATGGGCTCAGGTCACCTTTTATTTGAAATGTCATTTGGTGCCAGTATTTTTTAACTGCA	2280
Qy	2281	TAATAGCCTAACATGATTAATTTGAACTTAATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Db	2281	TAATAGCCTAACATGATTAATTTGAACTTAATTTACACATAGTTTGAAAAAAAAGACAAA	2340
Qy	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATATTTATTTTTTAAA	2400
Db	2341	AATAGTATTCAGGTGAGCAATTAGATTAGTATTTTCCACGTCACATATTTATTTTTTAAA	2400
Qy	2401	ACACAAATTTCTAAAGCTACACAAATACACAGGCGCTTAAAGCACAGTCTGATGACACA	2460
Db	2401	ACACAAATTTCTAAAGCTACACAAATACACAGGCGCTTAAAGCACAGTCTGATGACACA	2460
Qy	2461	TTTGGCAGTTTAAATAGATTTACTCAAGAAATTTTTTAAGAACTGTAATTTATTTTTTAA	2520
Db	2461	TTTGGCAGTTTAAATAGATTTACTCAAGAAATTTTTTAAGAACTGTAATTTATTTTTTAA	2520
Qy	2521	ATGGTGTTTTTATCAAGGGACCTTTGAACATGTTTTGTATGTTAAATCCAAAGTAATGC	2580
Db	2521	ATGGTGTTTTTATCAAGGGACCTTTGAACATGTTTTGTATGTTAAATCCAAAGTAATGC	2580
Qy	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACACTGTTTTCACTGTAATTTTGTATCA	2640
Db	2581	TTCAATCAGATAGTTCTTTTTTCAAGTTCAATACACTGTTTTCACTGTAATTTTGTATCA	2640
Qy	2641	AAATCAATGTCAAGTACCAAACTCTTAATGTATGTGTCATTTAACTCTGCCGTGAGACTT	2700
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Qy	2701	TCAGTGCACTGTATATAGAAGTCTAAACACACACTTAAGAGAAAAAGATCGAAATTTTCAG	2760
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Qy	2761	ATGATTCGGAATTTTCATTCAGGTATTTGTAATAGTCACATATATATGTATATACATAT	2820
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Db	2881	TTCCCTTTTCCATATAGGAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAGT	2940
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Db	3001	TCAGTATGAAGCTTAACCTCCCAACCCAAACATCTCCCTCCACATTTGTCAACATTTCAAAG	3060
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Db	3061	GGCCACAGTGACTTTTGTCTGGGCAATTTTCCAGATGTTTACAGACTGTGAGTACAGCAG	3120
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D	b	3121	AAAACTCTTTTACTAGTGTGTGTGTATATATAAAACAATGTAAATTCCTTTAGCCC	3180
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D	b	3181	ATTTTCTTAGACTGTCCTGTGGGAATATATTGTGTGTGTCATATATCATGTGTGTGAT	3240
Q	y	3241	GGTATGTATGGATTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
D	b	3241	GGTATGTATGGATTAATCTAATCTAATAATTGTGCCCGCAGTTGTGCCAAAGTGCATA	3300
Q	y	3301	GTCGTAGCTAAATCTAGGTGATTTGTCATCATGACAACTGCCTCAGTCCATTTTAACC	3360
D	b	3301	GTCGTAGCTAAATCTAGGTGATTTGTCATCATGACAACTGCCTCAGTCCATTTTAACC	3360
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D	b	3361	TGTAGCAACCTTCGCAATTCATAATCTTGTAATCATGTACCATTACAAATGGGATATA	3420
Q	y	3421	AGAGCGAGCTGGAAGCAGATGAGCTGTGGACTAGCAATATPAGGTTTGTGTGGTTGGT	3480
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RESULT 2	
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DEFINITION	cDNA encoding endothelin receptor, ERA-receptor.
ACCESSION	E07649
VERSION	E07649.1 GI:2175784
	4105 bp RNA linear PAT 29-SEP-1997

JP 1994157595-A/1.
SOURCE Homo sapiens.
-ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4105)
AUTHORS Imura, H., Nakao, I. and Nakanishi, S.
TITLE HUMAN ENDOTHELIN RECEPTOR
JOURNAL Patent: JP 1994157595-A 1 03-JUN-1994;
SHIONOGI & CO LTD
COMMENT OS Homo sapiens (human)
PN JP 1994157595-A/1
PD 03-JUN-1994
PF 12-JUL-1991 JP 1991172828
PI IMURA HIROO, NAKAO ICHIKAZU, NAKANISHI SHIGETADA PC
C07K13/00, C12N5/10, C12N15/12, C12P21/02, (C12N5/10, C12R1:91), PC
(C12P21/02,
PC C12R1:91);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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FEATURES
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BASE COUNT 1138 a 859 c 845 g 1263 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GAATTCGGCGCGCTCTTGGGTCGCCAGAGTGGAGTGGAGGCTGGAGCTTTGGGAGG 60
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1 GAATTCGGCGCGCTCTTGGGTCGCCAGAGTGGAGTGGAGGCTTTGGGAGG 60
61 AGACGGGAGGACAGACTGGAGGCGGTCTCCCGGAGTTTCTTTTCGTCGAGCCCT 120
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301 CGGAGCCGGGACACCGGCCACCTCCGCGCCACCCACCTCGCTTTCTCCGGGTTCTC 360

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Db 901 TAAGCTGTGGCTGGCGCTGCCCTTTTCATCACAATGACTTTGGCGTATTTCTTTGGCAA 960
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ACCESSION X61950
VERSION X61950.1 GI:288312
KEYWORDS endothelin-1 receptor.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hosoda, K., Nakao, K., Hiroshi-Arai, Suga, S., Ogawa, Y., Mukoyama, M.,
Shirakami, G., Saito, Y., Nakanishi, S. and Imura, H.
Cloning and expression of human endothelin-1 receptor cDNA
FEBS Lett. 287 (1-2), 23-26 (1991)
91348221
PUBMED 1652463

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ORIGIN

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IDS#5

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VERSION S57498.1 GI:298319
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REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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Arai,H., Nakao,K., Hosoda,K., Ogawa,Y., Nakagawa,O., Komatsu,Y. and
Imura,H.
Molecular cloning of human endothelein receptors and their
expression in vascular endothelial cells and smooth muscle cells
Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)
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PUBMED 1291713
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 128422] from the original journal article.
This sequence comes from Fig. 5.
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 VERSION D90348.1 GI:219649
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 AUTHORS Hosoda,K., Nakao,K., Hiroshi-Arai, Suga,S., Ogawa,Y., Mukoyama,M.,
 Shirakami,G., Saito,Y., Nakanishi,S. and Imura,H.
 TITLE Cloning and expression of human endothelin-1 receptor cDNA
 JOURNAL PERS Lett. 287 (1-2), 23-26 (1991)
 MEDLINE 91348221
 COMMENT These data kindly submitted in computer readable form by: kazuwa Nakao
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 Kyoto University School of Medicine
 54 Shogoin Kawahara-cho
 Sakyo-ku, Kyoto 606
 Japan
 Phone: 075-751-3170
 Fax: 075-771-9452
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S45956

LOCUS

S45956

ACCESSION

VERSION

S45956.1

GI:257375

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 3305)

AUTHORS

3305 bp mRNA linear PRI 08-MAY-1993

[human, placenta, mRNA, 3305 nt].

S45956

S45956

S45956.1

GI:257375

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

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AUTHORS

Liu, E.C., Bogosian, E.A., Brinson, E. and Runge, M.S.

TITLE Cloning and expression of a human endothelin receptor: subtype A
JOURNAL Am. J. Med. Sci. 304 (4), 231-238 (1992)
MEDLINE 93035452
PUBMED 1415318
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 115436] from the original journal article.
 This sequence comes from Fig. 2.

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VERSION BC022511.1 GI:18490297
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2705)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 32 Row: j Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503464.

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RESULT 8
HUMETAR8

LOCUS	HUMETAR8	2595 bp	DNA	linear	PRI 29-MAY-2002			
DEFINITION	Human DNA for endothelin-A receptor, exon 8 and 3' flanking region.							
ACCESSION	D1151							
VERSION	D1151.1	GI:219628						
KEYWORDS	G protein-coupled receptor; endothelin; endothelin-A receptor; endothelium; smooth muscle.							
SEGMENT	8 of 8							
SOURCE	Homo sapiens DNA, clone_lib.lambda EMBL3 and lambda EMBL3SP6/T77.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
	1 (bases 1 to 2595)							
	Hosoda,K., Nakao,K., Tamura,N., Arai,H., Ogawa,Y., Suga,S., Nakanishi,S. and Imura,H.							
	Organization, structure, chromosomal assignment, and expression of the gene encoding the human endothelin-A receptor							
AUTHORS	J. Biol. Chem. 267 (26), 18797-18804 (1992)							
TITLE	92406798							
JOURNAL	2 (bases 1 to 2595)							
MEDLINE	Hosoda,K.							
REFERENCE	Direct Submission							
AUTHORS	Submitted (18-MAY-1992) Kiminori Hosoda, Kyoto University School of Medicine, Department of Medicine; 54 Shogoin Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan (Tel:075-751-3170, Fax:075-771-9452)							
TITLE	Submitted (18-MAY-1992) to DDBJ by:							
JOURNAL								
COMMENT								

Phone: 075-751-3170
Fax: 075-771-9452

FEATURES	SOURCE
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3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10

CDS

CDS

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intro

exon

1104

polymer

COUNT

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stitch

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[illegible]

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RESULT 9
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FINITION Homo sapiens BAC clone RP11-752L20 from 4, complete sequence.
ACCESSION AC093908 AC067873
VERSION AC093908.3 GI:16497272
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164920)
Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
2 (bases 1 to 164920)
Paulson,E., Cotton,M. and Creason,K.
TITLE The sequence of Homo sapiens BAC clone RP11-752L20
JOURNAL Unpublished (2001)
3 (bases 1 to 164920)
Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 164920)
Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 164920)
Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 164920)
Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 5, 2002 this sequence version replaced gi:15778805.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0752L20
Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-56E3. Actual start of this clone is at base position 1 of RP11-752L20; actual end is at base position 164920 of RP11-752L20.

Data from AC083898 was used to finish this clone, AC093908.

The sequence of AC067873 has been incorporated into AC093908.

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3362 GTAGCAACCTTCTGCAATTCATAATCTTGTAACTGTATCATGTTACCATTACAAATGGGATATA 3421
Db 95094 GTAGCAACCTTCTGCAATTCATAATCTTGTAACTGTATCATGTTACCATTACAAATGGGATATA 95153
QY 3422 GAGCAGCGTGAAGCAGATGAGCTGTGGACTAGCAATATAGGGTTTGTGTTGGTTGGTT 3481
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QY 3602 GTCTGATATTTCTTACAGCTTCCCGCAGACAGATTTGCTGATAATAAATAGGTAAGATAA 3661
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QY 3722 AAGGCTAAGAAGTACTGCCCTTTTGTGTGTAGCACTCAAACTATATATCCACTGGCGC 3781
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QY 3962 AACTGTGGTTTACTAGCAGGAATATTTCCAAATTTTACCTTTTACTACATCTTTTCAACAA 4021
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QY 4022 GTAACCTTCTAGAAATGAGCCAGAACCCAGGCCCTGAGTTGGCAGTGGCCCATTAAGTGT 4081
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QY 4082 AAAATAAAGTTTACAGAAACCTT 4105
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RESULT 10
G06463
LOCUS human STS WI-7226, sequence tagged site.
DEFINITION G06463
ACCESSION G06463
VERSION G06463.1 GI:859708
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens STS derived from sequences in dbEST and the Unigene collection.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2337)
AUTHORS Hudson, T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
JOURNAL Unpublished (1995)
COMMENT

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: GATCGAATTTTTCAGATGATTCG
Primer B: AAATGCCAGCAAAAGTCAC
STS size: 343
PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:

2: 1.5 mM
50 mM
~HCL: 10 mM
9.3

Prepared with primer pairs derived from D90348 -- Unigene.

Location/Qualifiers

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/organism="Homo sapiens"

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/db_xref="taxon:9606"

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978. .13

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a	407	c	407	g	784	t	45	others
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ORIGIN

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QY	1769	CCACCCCTTAGAGACACTCCTCGGTACTCCCAATATCTCTCGGAGAAAAAATCACAGG	1828		
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QY	1829	CAACTGTGACTCCGGGAATCTCTCTCGATCCCTCTCTTAATTCACCTCCACACCCA	1888		
DB	61	CAACTGTGACTCCGGGAATCTCTCTCGATCCCTCTCTTAATTCACCTCCACACCCA	120		
QY	1889	AGAGAAATGCTTCCAAAACCGAAGTAGACTGGTTATCCACCCACACACTCTACGA	1948		
DB	121	AGAGAAATGCTTCCAAAACCGAAGTAGACTGGTTATCCACCCACACACTCTACGA	180		
QY	1949	ATCTGACTCTCTTAATTGATCTAAATTTACATATTTCTCGGTGTGTATTCAGCAGCTAAAA	2008		
DB	181	ATCTGACTCTCTTAATTGATCTAAATTTACATATTTCTCGGTGTGTATTCAGCAGCTAAAA	240		
QY	2009	ATGTGGGAGCTGGGGAGATGAAGACTGTTAAATGAACCAAGAGATTTTACTACT	2058		
DB	241	ATGTGGGAGCTGGGGAGATGAAGACTGTTAAATGAACCAAGAGATTTTACTACT	300		
QY	2069	TTTGCATGAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGTGGTGAATG	2128		
DB	301	TTTGCATGAAATAGAGCTTTCAAGTACATGGCTAGCTTTTATGGCAGTTCTGTGGTGAATG	360		
QY	2129	TTCAATGGGAAGCTGGTCAACATGAACCTTTAGAGATTTAAGCAAGATTTTCTACTTTT	2188		
DB	361	TTCAATGGGAAGCTGGTCAACATGAACCTTTAGAGATTTAAGCAAGATTTTCTACTTTT	420		
QY	2189	TTAAGTCATTTTCTCTCAGTCAACCAACAAATATGGCTCAGCTCACTTTTATTTCGA	2248		
DB	421	NNNNNNNNNNNGTCTTCAGCAGCAACAAATATGGCTCAGCTCACTTTTATTTCGA	480		
QY	2249	ATGTCATTTGGTGGCAGTATTTTTAACTGCATTAATAGCCTTAACATGATTTATTTGAACCT	2308		
DB	481	ATGTCATTTGGTGGCAGTATTTTTAACTGCATTAATAGCCTTAACATGATTTATTTGAACCT	540		
QY	2309	ATTTTACACATAGTTTGAAGAAAAAAGACAAAAATAGTATTCAGGTGAGCAATTTAGATTA	2368		
DB	541	ATTTTACACATAGTTTGAAGAAAAAAGACAAAAATAGTATTCAGGTGAGCAATTTAGATTA	600		
QY	2369	GTATTTTCCAGCTCAGCTATTTATTTTTTAAACACAAAAATCTAAAGCTACACAAATAC	2428		
DB	601	GTATTTTCCAGCTCAGCTATTTATTTTTTAAACACAAAAATCTAAAGCTACACAAATAC	660		
QY	2429	TACAGGCCCTTAAAGCACAGCTCTGATGACACATTTGGCAGTTTAAATAGATTTACTCAAA	2488		
DB	661	TACAGGCCCTTAAAGCACAGCTCTGATGACACATTTGGCAGTTTAAATAGATTTACTCAAA	720		
QY	2489	GAATTTTTTAAAGAACTGATTTTATTTTTTAAATGGTGTATTTATTAAGGAGCCTTGA	2548		

QY	1381	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGTGGTTGAATTTTGCTCTTTGCTG	1440
Dg	970	GCAGCGTCGAGAAGTGGCAAAACAGTTTTCTGTGGTTGAATTTTGCTCTTTGCTG	1029
QY	1441	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACACTGTATACGAAAAATGGACAAGAA	1500
Dg	1030	GTTCCCTCTTCACTTAAGCCGTATATTGAAGAAAACACTGTATACGAAAAATGGACAAGAA	1089
QY	1501	CCGATGTGAATTTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTCGSCAAC	1560
Dg	1090	CCGATGTGAATTTACTTAGTTTCTTACTGCTCATGGATTACATCGGTATTAACTTCGSCAAC	1149
QY	1561	CATGAATTCATGTATAAACCOCATASCTCTGTATTGTTGAGCAAGAAAATTTAAAAATTTG	1620
Dg	1150	CATGAATTCATGTATAAACCOCATASCTCTGTATTGTTGAGCAAGAAAATTTAAAAATTTG	1209
-Qy	1621	TTCAGTTCATGCCCTCTGCTGTGCTGTATTACAGTCCAAAAGTCTGTATGACCTCGGTCCC	1680
Jb	1210	TTCAGTTCATGCCCTCTGCTGTGCTGTATTACAGTCCAAAAGTCTGTATGACCTCGGTCCC	1269
QY	1681	CATGAACGGAACACAGCATTCCAAGTGAAGAACCCACGATCAAACACACACAGACCG	1740
Dg	1270	CATGAACGGAACACAGCATTCCAAGTGAAGAACCCACGATCAAACACACACAGACCG	1329
QY	1741	GAGCAGCCATAAGGACACATGAAGTACACACCCCTTGAAGCACTCTCTCGTACTCCCCAT	1800
Dg	1330	GAGCAGCCATAAGGACACATGAAGTACACACCCCTTGAAGCACTCTCTCGTACTCCCCAT	1389
QY	1801	AATCCTCTCGGAGAAAAAATCACAAAGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1860
Dg	1390	AATCCTCTCGGAGAAAAAATCACAAAGCAACTGTGACTCCGGGAATCTCTTCTCTGATC	1449
QY	1861	CTTCTCTCTTAATTCACCTCCACACCCCAAGAAAGTCTTTCCAAAACCCGAA-GSTAG	1919
Dg	1450	CTTCTCTCTTAATTCACCTCCACACCCCAAGAAAGTCTTTCCAAAACCCGAAAGGSTAG	1509
QY	1920	ACTGTTTATCCACCACCAACATCTACCAATCGTACTTCTTAATGATCTAAATTTACAT	1979
Dg	1510	ACTGTTTATCCACCACCAACATCTACCAATCGTACTTCTTAATGATCTAAATTTACAT	1569
QY	1980	ATTCTGCGTGTGATTTCAGCAGCTAAAAAATGGTGGGAGCTGGGGGAGAAATGAAGACTGT	2039
Dg	1570	ATTCTGCGTGTGATTTCAGCAGCTAAAAAATGGTGGGAGCTGGGGGAGAAATGAAGACTGT	1629
QY	2040	TAAATGAACACAGAGGATATTTACTACTTTTGCATGAAATAGAGCTTTTCAAGTACATG	2099
Jb	1630	TAAATGAACACAGAGGATATTTACTACTTTTGCATGAAATAGAGCTTTTCAAGTACATG	1689
QY	2100	GCTAGCTTTTATGCGAGTCTGGTGAATGTTCATGGGAACCTGGTCACCATGAACCTTTA	2159
Dg	1690	GCTAGCTTTTATGCGAGTCTGGTGAATGTTCATGGGAACCTGGTCACCATGAACCTTTA	1749
QY	2160	GAGATTACGACAAAGATTCTTCTACTTTTTTAAAGTGA-TTTTGTGCTCTCAGCCCAACA	2218
Dg	1750	GAGATTACGACAAAGATTCTTCTACTTTTTTAAAGTGA-TTTTGTGCTCTCAGCCCAACA	1809
QY	2219	CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	2268
Dg	1810	CAATATGGGCTCAGGTCACTTTTATTTGAAATGTCATTTGGTGCCAGTAT	1859
RESULT 12			
BTBETREC			
LOCUS	BTBETREC	3216 bp	mRNA linear MAM 20-FEB-1991
DEFINITION	Bovine mRNA for endothelin receptor.		
ACCESSION	X57865		
VERSION	X57865.1	GI:121	
KEYWORDS	endothelin receptor.		
SOURCE	cow.		
ORGANISM	Bos taurus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		

QY	2698	CTTTCACTGCTAGTATAGAAAGCTTAAACACACACCTTAAGAGAAAAGATCGAAT-TTTT	2756
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QY	2757	TCAGATGATTCGGAAATTTTCATTCAGG-----TATTTGTAATAGTGACATATATATG--	2809
Db	2726	TCAGAGGATTTGGAAATTCCTCATTCAGGTTTATTTTGGTAATAGTACGGTATATATGTG	2785
QY	2810	-----TATATACAT	2818
Db	2786	TGTGTCAGATATACACATATGTATCGTGTACATATATACATGCATATACATATACAT	2845
QY	2819	ATCACTCCCTATTCCTTAAATTTTGTAAATGTTAACTGGCAGTAAAGTCTTTTTTGTAT	2878
Db	2846	GTATGTATATATTCCTTTGCTTCCTTTTAAATGTTAACTGGCAGTGAGACTTTTTTGGT	2905
QY	2879	CATTCCCTTTTC-----CATATAGGAACATATTTTGAAGTGGCCAGATGAGTTAT	2931
Db	2906	CATTCCCTTTTCCACGGAGGAATATGGAAACATATTTCAAAGTGGCCAGCTGAGTTAT	2965
QY	2932	CATGTCAGTGAATAATATACCCACAAATGCCACCACTAACTTAAAGCATTCCTCACTTC	2991
Db	2966	TGTGTCATGAATATATTAATCTACTCCAGATGCCGCCATGAATTA--GGTCTTTCATGTC	3024
QY	2992	TGCGGGTTTTCAGTATGAACCTAACTCCCCACCAACATCTCCCTCCCAATGTGCACC	3051
Db	3025	CCTGGGTTTTTCAGTATGAACCTAAATGCCITCCCTACCCACACTC-CTCACATGGTCACC	3083
QY	3052	ATTTCAAAAGGCCACAGTGAATTTGCTGGGCAATTTTCCAGATGTTTACAGACTGTGA	3111
Db	3084	ATTTCAAAAGGCCCGCAGTGACTTCTGCTGGGCGTTTTTCCACGATGTTTACAAACTGTGA	3143
QY	3112	GTACAGCAGAAATCTTTTACT-----AGTGTGTGTGTATATATATAAACAATTTGTA	3166
Db	3144	TTGCAGCAGCAATCTTTTACTGTGTATATAAATATATGATATATAAACAACACTGTAA	3203
QY	3167	ATTTCTTTTAGCC	3179
Db	3204	ATTTCTTTTAGCC	3216
RESULT	13		
LOCUS	S67127	1661 bp mRNA linear	PRI 07-MAY-1993
DEFINITION	S67127	endothelin ETA receptor [human, placenta, mRNA, 1661 nt].	
ACCESSION	S67127		
VERSION	S67127.1	GI:239560	
KEYWORDS		Homo sapiens placenta.	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 (bases 1 to 1661)	
AUTHORS		Cyr,C., Huebner,K., Druck,T. and Kris,R.	
TITLE		Cloning and chromosomal localization of a human endothelin ETA receptor	
JOURNAL		Biochem. Biophys. Res. Commun. 181 (1), 184-190 (1991)	
MEDLINE		92068188	
PUBMED		1459806	
REMARK		GenBank staff at the National Library of Medicine created this entry [NCBI Gibbsq 67127] from the original journal article. This sequence comes from Fig 1.	
		Map location: chromosome 4.	
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BASE COUNT	453 a	386 c	349 g	473 t	
ORIGIN					
Query Match	38.0%	Score 1560.2;	DB 9;	Length 1661;	
Best Local Similarity	99.7%;	Pred. No. 0;			
Matches 1584; Conservative	0;	Mismatches	3;	Indels	2; Gaps 2;
Qy	421	AAAAAGTGAAGGTGTA AAAAGC - AGCA AAGTGCAAT AAGAGATA TTT CCTCAA ATTTGCC	479		
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Qy	480	TCAAGATGGA AACCC TTGGCTCAGGGCATCCTTTTGGCTGGCA CTGGTGGATGTGTAA	539		
Db	133	TCAAGATGGA AACCC TTGGCTCAGGGCATCCTTTTGGCTGGCA CTGGTGGATGTGTAA	192		
Qy	540	TCAGTGA TAATCC TGAGAGATACAGCAACAATTAAGCAATCATGTGATGATTTCACCA	599		
Db	193	TCAGTGA TAATCC TGAGAGATACAGCAACAATCTAAGCAATCATGTGATGATTTCACCA	252		
Qy	600	CTTTTCTGGGCACAGAGCTCAGCTTCCTGGTTACCAC TCATCAACCCACTAA TTTGGTCC	659		
Db	253	CTTTTCTGGGCACAGAGCTCAGCTTCCTGGTTACCAC TCATCAACCCACTAA TTTGGTCC	312		
Qy	660	TACCAGCAATGGCTCAATGCAACAAC TATGCCACACAGCAGACTAAA ATTACTTCAGTT	719		
Db	313	TACCAGCAATGGCTCAATGCAACAAC TATGCCACACAGCAGACTAAA ATTACTTCAGCTT	372		
Qy	720	TCAAATACATTAACACTGTGATATCTTG TACTATTTTCATCGTGGGAATGGTGGGAATG	779		
Db	373	TCAAATACATTAACACTGTGATATCTTG TACTATTTTCATCGTGGGAATGGTGGGAATG	432		
Qy	780	CAACTCTGCTCAGGATCATTTTACCAGAACAATGTATGAGGAATGGCCCCAACCGCTGA	839		
Db	433	CAACTCTGCTCAGGATCATTTTACCAGAACAATGTATGAGGAATGGCCCCAACCGCTGA	492		
Qy	840	TAGCAGTCTTGGCCCTGGAGACCTTATCTATGTGGTCA TTGATCTCCCTATCAATGTAT	899		
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Db	553	TTAAGTCTCTGGCTGGGGCTGGGCTTTTGATACAATGACTTTGGGCTATTTCTTTGCA	612		
Qy	960	AGCTGTTC CCCC TTTTGCAGAAAGTCCCTGGTGGGGATCACCGTCTCAACCTCTGC GCTC	1019		
Db	613	AGCTGTTC CCCC TTTTGCAGAAAGTCCCTGGTGGGGATCACCGTCTCAACCTCTGC GCTC	672		
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Qy	1140	CTGAAGCGA TTGGCTTCGTTCATGTG TACCCCTTTGAATATAGGGGTGAACAGCATAAAA CCT	1199		
Db	793	CTGAAGCGA TTGGCTTCGTTCATGTG TACCCCTTTGAATATAGGGGTGAACAGCATAAAA CCT	852		
Qy	1200	GTA TGCTCAATGCCACATCAAAATTCATGGAGTCTT ACCAAGATGTAAAGACTGTGTGGC	1259		
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QY 1320 CTTGTGAGATGTTGAACAGAGAAATGGCAGCTTGAGATTCGCCCTCAGTGAACATCTTA 1379
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QY 1800 TAATCCTCTCGGAGAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGAT 1859
Db 1453 TAATCCTCTCGGAGAAAAATCAAGGCAACTGTGACTCCGGGAATCTCTTCTCTGAT 1512
QY 1860 CTTCTCTCTTAATTAATCACTCCACACCAAGAAATGCTTTCCAAAACGCAAGGTAG 1919
Db 1513 CTTCTCTCTTAATTAATCACTCCACACCAAGAAATGCTTTCCAAAACGCAAGGTAG 1572
QY 1920 ACTGGTTTATCCACCAACATCTACGAATCGTACTTC-TTTAATGATCTAATTTACA 1978
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QY 1979 TATTCTGGTGTGTTGATTCAGCACTAAA 2007
Db 1633 TATTCTGGTGTGTTGATTCAGCACTAAA 1661
RESULT 14
S81539
LOCUS S81539 1359 bp mRNA linear PRI 03-AUG-1996
DEFINITION endothelin-A receptor-ET-AR [human, lung, mRNA Partial, 1359 nt].
ACCESSION S81539
VERSION S81539.1 GI:1478475
KEYWORDS
SOURCE Homo sapiens lung.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1359)
AUTHORS Miyamoto, Y., Yoshimasa, T., Arai, H., Takaya, K., Ogawa, Y., Itoh, H.
and Nakao, K.
TITLE Alternative RNA splicing of the human endothelin-A receptor
generates multiple transcripts
JOURNAL Biochem. J. 313 (Pt 3), 795-801 (1996)
MEDLINE 96190719
PUBMED 8611157

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gbbseq 176815] from the original journal article. This sequence comes from Fig. 3A.

FEATURES
source 1. .1359 Location/Qualifiers
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gene 1. .1359
CDS 1. .1284
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GenBank staff at the National Library of Medicine created this entry [NCBI gbbseq 176815] from the original journal article. This sequence comes from Fig. 3A.

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AUTHORS Elshourbagy, N.A., Korman, D.R., Wu, H.L., Sylvester, D.R., Lee, J.A.,
Nuthalaganti, P., Bergsma, D.J., Kumar, C.S. and Nambip.
TITLE Molecular characterization and regulation of the human endothelin
receptors
J. Biol. Chem. 268 (6), 3873-3879 (1993)
MEDLINE 93179382
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